

Access DB#

47046

SEARCH REQUEST FORM

Scientific and Technical Information Center

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Art Unit: _____ Phone Number 30 _____ Serial Number: _____
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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____
Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

STAFF USE ONLY

| | Type of Search | Vendors and cost where applicable |
|---------------------------------------|--------------------------|---------------------------------------------|
| Searcher: <u>D. Schreiber</u> | NA Sequence (#) _____ | STN _____ |
| Searcher Phone #: <u>308-4292</u> | AA Sequence (#) <u>4</u> | Dialog _____ |
| Searcher Location: <u>CM1 12E18</u> | Structure (#) _____ | Questel/Orbit _____ |
| Date Searcher Picked Up: <u>7/23</u> | Bibliographic _____ | Dr. Link _____ |
| Date Completed: <u>7/23</u> | Litigation _____ | Lexis/Nexis _____ |
| Searcher Prep & Review Time: <u>7</u> | Fulltext _____ | Sequence Systems <u>CompuGen Ig @FastDB</u> |
| Encal Prep Time _____ | Patent Family _____ | WWW/Internet _____ |
| Line Time <u>15</u> | Other _____ | Other (specify) _____ |

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K19155 Fin 47046

From: Zeman, Mary
 Sent: Wednesday, July 18, 2001 10:49 AM
 To: STIC-Biotech/ChemLib
 Subject: SEQ Search. 09/636801

CRFE
ALL

Please search SEQ ID NO: 392 in all files but not pending files.

Please search SEQ ID NO: 392 against the following parent files (For priority):
 09/617747; 09/404879; 09/338933; 09/216003 and 09/215681

Paper printout please

Thank you

Mary Zeman

Examiner, 1631

Office 12A17

Mailbox 12D01

Elected Gpl clms
 1, 2, 9-12, 21, 23, 24 + 69-72
 SEQ ID NO 392 paper #9
 7/16/01
 No args.

NUCLEO SEQ 391 "provide full length sequences incorporating certain", p53

392 Not in Table @ p50-53 proteins encoded by OSE

No protein in '003 + 68

p53 = OSE
 seq 392 = "b" form

OSE polyclonal Ab p54
 used 20-mers of OSE

1/6 ovarian tissue samples was positive for OSE p55
 No controls

p56 FACS sorting - what kind of cells?
 Breast cancer HEK293
 Not MB415? or

1/55
 10/16/00

clms 9-12
 vaccine

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 10:11:58 ; Search time 11.22 Seconds

(without alignments)
943,400 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574

Sequence: 1 HASAHASGROQLHSASTQI.....SSFAISWALLPLSPYIMLK 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 215.5 | 13.7 | 526 | 1 | BUTY_BOVIN |
| 2 | 211.5 | 13.4 | 526 | 1 | BUTY_HUMAN |
| 3 | 178.5 | 11.3 | 524 | 1 | BUTY_MOUSE |
| 4 | 163.5 | 10.4 | 299 | 1 | CD80_RABBIT |
| 5 | 152 | 9.7 | 245 | 1 | MOG_RAT |
| 6 | 150.5 | 9.6 | 329 | 1 | MOG_MOUSE |
| 7 | 147.5 | 9.4 | 329 | 1 | CD86_HUMAN |
| 8 | 147.5 | 9.4 | 330 | 1 | CD86_RABBIT |
| 9 | 147.5 | 9.4 | 558 | 1 | Y653_HUMAN |
| 10 | 144 | 9.1 | 247 | 1 | MOG_HUMAN |
| 11 | 143.5 | 9.1 | 309 | 1 | CD86_MOUSE |
| 12 | 140.5 | 8.9 | 246 | 1 | MOG_BOVIN |
| 13 | 135 | 8.6 | 761 | 1 | NCA2_HUMAN |
| 14 | 135 | 8.6 | 848 | 1 | NCA1_HUMAN |
| 15 | 132.5 | 8.4 | 853 | 1 | NCA1_BOVIN |
| 16 | 131 | 8.3 | 1091 | 1 | NCA1_CHICK |
| 17 | 130.5 | 8.3 | 725 | 1 | NCA2_MOUSE |
| 18 | 130.5 | 8.3 | 1115 | 1 | NCA1_MOUSE |
| 19 | 128.5 | 8.2 | 858 | 1 | NCA1_RAT |
| 20 | 126.5 | 8.0 | 1088 | 1 | NCA1_XENLA |
| 21 | 125.5 | 8.0 | 298 | 1 | VEJA_HUMAN |
| 22 | 124 | 7.9 | 306 | 1 | CD80_MOUSE |
| 23 | 123 | 7.8 | 365 | 1 | CXAR_MOUSE |
| 24 | 121 | 7.7 | 1010 | 1 | COMT_CHICK |
| 25 | 120 | 7.6 | 215 | 1 | CIB2_RAT |
| 26 | 120 | 7.6 | 288 | 1 | CD80_HUMAN |
| 27 | 120 | 7.6 | 333 | 1 | AMAL_DROME |
| 28 | 120 | 7.6 | 365 | 1 | CXAR_HUMAN |
| 29 | 119 | 7.6 | 323 | 1 | DIM1_CAEEL |
| 30 | 115.5 | 7.3 | 1092 | 1 | NCA2_XENLA |
| 31 | 113.5 | 7.2 | 1336 | 1 | VCRL_RAT |
| 32 | 113.5 | 7.2 | 1461 | 1 | NEO1_HUMAN |
| 33 | 113 | 7.2 | 359 | 1 | LACH_DROME |

ALIGNMENTS

RESULT 1

| ID | Buty_BOVIN | STANDARD | PRT | 526 AA. |
|----|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|-----|---------|
| AC | P18892; O18955; O18959; | | | |
| DT | 01-NOV-1990 (Rel. 16, Created) | | | |
| DT | 15-JUL-1998 (Rel. 36, Last sequence update) | | | |
| DT | 30-MAY-2000 (Rel. 39, Last annotation update) | | | |
| DE | BUTYRPHILIN PRECURSOR (BT). | | | |
| GN | BTN. | | | |
| OC | Bos taurus (Bovine). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; | | | |
| OC | Bovidae; Bovinae; Bos. | | | |
| OX | NCBI_TaxID=9913; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A., AND SEQUENCE OF 27-47. | | | |
| RA | MEDLINE=90354441; PubMed=2387867; | | | |
| RT | Jack L.T.W., Mather I.H.; | | | |
| RT | "Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein expressed in mammary tissue and secreted in association with the milk-fat globule membrane during lactation."; | | | |
| RT | J. Biol. Chem. 265:14481-14486(1990). | | | |
| RL | [2] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RP | STRAIN=HOLSTEIN-FRIESIAN; | | | |
| RA | Daye H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V., | | | |
| RT | Mather I.H., Wilkins R.V.; | | | |
| RT | Submitted (May-1997) to the EMBL/GenBank/DBJ databases. | | | |
| RL | [3] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RP | Tissue=Blood; | | | |
| RA | Seyfert H., Luethen F.; | | | |
| RT | Submitted (Mar-1997) to the EMBL/GenBank/DBJ databases. | | | |
| RL | [4] | | | |
| RN | CARBOHYDRATE-LINKAGE SITES. | | | |
| RP | MEDLINE=95293916; PubMed=775382; | | | |
| RA | Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.; | | | |
| RT | "Site-specific glycosylation of bovine butyrophilin."; | | | |
| RT | J. Biochem. 117:147-157(1995). | | | |
| RL | [5] | | | |
| RN | FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA MEMBRANE. | | | |
| RP | - SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE (BY SIMILARITY). | | | |
| RP | - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. | | | |
| RP | - TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION. | | | |
| RP | - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY. | | | |
| RP | - SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP). | | | |
| RP | CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way | | | |

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CC or send an email to license@sib-sib.ch).

DR EMBL; M35551; AAB39766.1; -
DR EMBL; AF005497; AAB62889.1; -
DR EMBL; Z93323; CAB07533.1; -
DR PIR; A37821; A37821.
DR InterPro; IPR000107; -
DR InterPro; IPR003006; -
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00047; Ig; 1.
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1
FT CHAIN 26
FT DOMAIN 27 526
FT TRANSMEM 27 242 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 243 269 POTENTIAL.
FT DOMAIN 270 526 CYTOPLASMIC (POTENTIAL).
FT CARBOHD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
FT CARBOHD 215 215 N-LINKED (GLCNAC. . .) (HYBRID).
FT CONFLICT 35 35 Q -> P (IN REF. 3).
FT CONFLICT 230 230 E -> D (IN REF. 1).
SQ SEQUENCE 526 AA; 59276 MW; A14126802BD19284 CRC64;

Query Match 13.7%; Score 215.5; DB 1; Length 526;
Best Local Similarity 24.5%; Pred. No. 3.8e-10;
Matches 48; Conservative 49; Mismatches 94; Indels 5; Gaps 4;

OY 75 IGEDGILSTCFEPDKILSDIYQWLKEGYLGVHFEKCKDLSRDEMRGRTRAVFADQ 134
Db 42 VGEDDELPCRLSPNBSAKGMELMRERKVPSPVRSQEGEGEMAEYRGVSLVEDH 101
OY 135 VVGNASLRKLVQQLTDAGTYKCYIITSKGNANLVEYTGAF-SMEPVNVYNASSE-T 192
Db 102 IAGSEVAVRIQGVKASDGEYCFRQDENYEALVHLKVALGSDPHSMQVQSGELQ 161
OY 193 LRCEAPRPFQPTVYVASOVDOGANFSEVSNFSPELSENVTMKVSVLYVNTINNTYSC 252
Db 162 LECTSVGWYPEPOVOM--RTRGEEFSPMSSESNDDEGLFTVRAVSIIRDSMKNV-SC 218
OY 253 MIENDIAKATGDIKYT 268
Db 219 CIRNLLGOEKEVEVS 234

RESULT 2
BUTY_HUMAN STANDARD; PRT; 526 AA.
AC Q13410;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BUTYROPHILIN PRECURSOR (BT).
GN BTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast; PubMed=8611614;
RX MEDLINE=96201696; PubMed=8611614;
RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
RT "Cloning and sequence analysis of human butyrophilin reveals a
RT potential receptor function."
RL Blochm. Biophys. Acta 1306:1-4(1996).
CC -1- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -1- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE DOMAIN. BELONGS TO THE ERM/MOG SUBFAMILY.
CC -1- SIMILARITY: STRONG, TO THE C-TERMINAL OF RET FINER PROTEIN (RFP).
CC
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DR EMBL; U39576; AAC50489.1; -
DR MIM; 601610; -
DR InterPro; IPR000107; -
DR InterPro; IPR003006; -
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00047; Ig; 1.
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1
FT CHAIN 26
FT DOMAIN 27 526
FT TRANSMEM 27 242 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 243 269 POTENTIAL.
FT CARBOHD 55 55 CYTOPLASMIC (POTENTIAL).
FT CARBOHD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 526 AA; 59004 MW; E9EACACF8DAF94D5 CRC64;

Query Match 13.4%; Score 211.5; DB 1; Length 526;
Best Local Similarity 26.6%; Pred. No. 8.1e-10;
Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;

OY 75 IGEDGILSTCFEPDKILSDIYQWLKEGYLGVHFEKCKDLSRDEMRGRTRAVFADQ 134
Db 42 VGEDDELPCRLSPNBSAEHLERKRVSPVAVLHRODREDAQOMPTKRAATLVQDG 101
OY 135 VVGNASLRKLVQQLTDAGTYKCYIITSKGNANLVEYTGAF-SMEPVNVYNASSE-T 192
Db 102 IAKGVAVLRIRGVRSDDGEYCFRQDGYEALVHLKVALGSDPHSMQVQSGELC 161
OY 193 LRCEAPRPFQPTVYVASOVDOGANFSEVSNFSPELSENVTMKVSVLYVNTINNTYSC 252
Db 162 LECTSVGWYPEPOVOM--RTSKGEKFPSTSE-SRNPDEGLFTVAASYIIRDTSPKNSC 218
OY 253 MIEN 256
Db 219 YLON 222

RESULT 3
BUTY_MOUSE STANDARD; PRT; 524 AA.
AC Q62556; P97392;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BUTYROPHILIN PRECURSOR (BT).
GN BTN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary gland;
RX MEDLINE=97148936; PubMed=8995761;
RA Ogg S.L., Komaragiri M.V.S., Mather I.H.;
RT "Structural organization and mammary-specific expression of the
RT butyrophilin gene."
RL Mamm. Genome 7:900-905(1996).
RN [2]

A:Molecule type: mRNA
A:Residues: 1-526 <TAV>
A:Cross-references: EMBL:U039576; NID:g1326082; PIDN:AAG50489.1; PID:g1326083

Query Match 13.4%; Score 211.5; DB 2; Length 526;
Best Local Similarity 26.6%; Pred.No.1.4e-08;
Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;

QY 75 IGEDGILSCFEPDIKLSIDIVIQWLKEGVLGVHEFEKSGKDELSEODEMFRGRTRAVFADQ 134
DB 42 VEDDELPELRSPNMASELELRMPFRKKVSPAVLVHRDREDAEQMPEYRGRATLVQDG 101
QY 135 VIVGNASLRKLVQLTDAGTYCYIITSKGNANLEYKTGAF-SMPEVNVVDYNASSE-T 192
DB 102 IAKGRALAIRGVRVSDDEYTCFFREDGSEALVHLKVALGSDPHISMVQENGCEIC 161
QY 193 LRCEAPRMPQPTVYVWASQVDGANSFSEVSNFSFELNSENVTKMVSVLVNTINTYSC 252
DB 162 LRCTSGWTPPEQVQW--RTSKGEKFPSTSE-SRNPDEGLFTVAASVILRDTSTKNVSC 218
QY 253 MIEN 256
DB 219 YIQN 222

RESULT 3
S65133
butyrophillin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S65133
R:Ishii, T.; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1245, 285-292, 1995
A:Title: Carboxy-terminal cytoplasmic domain of mouse butyrophillin specifically associat
A:Reference number: S65133; MUID:96125722
A:Accession: S65133
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-487 <ISH>
A:Cross-references: GB:S80642; NID:g1246078; PIDN:AAB35893.1; PID:g1246079

Query Match 10.9%; Score 171.5; DB 2; Length 487;
Best Local Similarity 22.4%; Pred.No.1.4e-05;
Matches 44; Conservative 51; Mismatches 92; Indels 9; Gaps 4;

QY 77 EDCILSCFEPPIKISDVIQWLKEGVLGVHEFEKSGKDELSEODEMFRGRTRAVFADQYI 136
DB 8 DDAELTCGSPNASESEYMLMFROTSTAVLLYRDGQEQGQMTKRGKATLTATAGLL 67
QY 137 VGNASLRKLVQLTDAGTYCYIITSKGNANLEYKTGAF-SMPEVNVVDYNASSE-TLR 194
DB 68 DGRATLLLRDVAFSDQGEKRCLEKNDDEFEAAVILKVAASDPOISMTVQENGEMELE 127
QY 195 CEAPRMPQPTVYVWASQVDGANSFSEVSNFSFELNSENVTKMVSVLVNTINTYSC 252
DB 128 CTSWSGWTPPEQVQWRT-----GNREMLPSTDSKKNHEGLFTVAVSMWISDSIKNSC 182
QY 253 MIENDIAKATGDIKYT 268
DB 183 CTQNTLLGGKREVEIS 198

RESULT 4
T09058
butyrophillin homolog - mouse (fragment)
N:Alternate names: butyrophillin-like protein
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: T09058
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc
submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09058
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-391 <ROW>
A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564946
A:Note: BAC 29N7
C:Genetics:
A:Map position: 17
A:Note: butyrophillin-like
A:Note: Intron positions not resolved (incomplete sequence)

Query Match 10.7%; Score 168.5; DB 2; Length 391;
Best Local Similarity 26.3%; Pred.No.1.9e-05;
Matches 52; Conservative 45; Mismatches 82; Indels 19; Gaps 8;

QY 76 GEDGILSCFEPDIKLSI-DVIQWLKEGVLGVHEFEKSGKDELSEODEMFRGRTRAVFADQ 134
DB 26 GREALIPCSVIPVMVNEEELRWYRNRPASAVALYRDQEQKREQMTEYSWRTSLVKDQ 85
QY 135 VIVGNASLRKLVQLTDAGTYCYIITSKGNANLEYKTGAF-SMPEVNV-DYNASSFT 192
DB 86 FHOGRTRAVRIQNIQASDSICVICHFMGQFHEALTELKVALMGSPVEVHIGPEDGVC 145
QY 193 LRCEAPRMPQPTVYVWASQVDGANSFSEVSNFSFELNSENV-----TMKVY--SVLYN 243
DB 146 VVCMNTSGWTPPEQVQWNRD--SRGEKFT----ASLEHGDAGLGRTERSLVYRROSSVKN 199
QY 244 VTINTYSCMIENDIAKA 261
DB 200 V-ICSTFNSILGEEKAMA 216

RESULT 5
I46690
CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C:Accession: I46690
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole
A:Reference number: I46689; MUID:95369849
A:Accession: I46690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <ISO>
A:Cross-references: GB:D49843; NID:g755096; PIDN:BA08643.1; PID:g755097
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 10.4%; Score 163.5; DB 2; Length 299;
Best Local Similarity 25.3%; Pred.No.3.2e-05;
Matches 73; Conservative 57; Mismatches 89; Indels 69; Gaps 19;

QY 40 ISITITLGAALILGFGISGRHSITVTVAAGNIGEDGILSCFEPDI-KLSDIVQW 98
DB 19 LCLLALAC---LHSSSGIS-----QVTK-----SYKEAALSCYRNSIDELAMKRIY 65
QY 99 IKEG--VIGLVHEFEKSGDELSEODEMFRGRTRAVFADQYVGNASLRKLVQLTDAGTYK 156
DB 66 QKDQGVLSII-----SGQVEVWPE--YKNRT--FPD--IINNLSIMILALRLSDKGYT 114
QY 157 CYIITSKGNANLEYKTGA-----FSMPV-----NVDYASSETLRCEAPRMPQPT 205
DB 115 C-VVCKNENGSPRRBHLTSVTLIRADPPVPSITDIGHDPNV--KRIRCSASGGFPPR 171
QY 206 VYVWASQVDGANSFSEVSNFSFELNSENVTKMVSVLV--VNTVTINTYSCMIENDIAKATGD 264
DB 172 LAM---MEDGELNAV--NTYVDQDLDTLTSVSELDERNTVNNHSIVCLIK-----YGE 221

OY 265 IKYTE-----SEIKRSHLOLNSKASICVSSFAISWALLPLSPYML 308
 Db 222 LSVSQRFPWSPKQEPIDLP-----FWVITPVSGALV 256

RESULT 6

T28137
 Ig V-region-like B-G antigen, isoform 2 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T28137
 R:Milne, S.; Kaufman, J.; Beck, S.
 Submitted to the EMBL Data Library, May 1998
 A:Description: DNA sequencing and analysis of the chicken major histocompatibility comp
 A:Reference number: Z20475
 A:Accession: T28138
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-339 <MIL>
 A:Cross-references: EMBL:AL023516; PIDN:CAA18959.1
 A:Experimental source: clone CB12
 C:Genetics:
 A:Gene: B-G 2
 A:Map position: 16
 A:Introns: 34/1; 148/1; 183/1; 189/1; 196/1; 203/1; 210/1; 217/1; 224/1; 231/1; 239/1; 2

Query Match 9.6%; Score 151; DB 2; Length 339;
 Best Local Similarity 21.7%; Pred. No. 0.00034;

Matches 56; Conservative 46; Mismatches 90; Indels 66; Gaps 10;

OY 63 SITVTYVASAGNIGEDGILSCFEP--DIKLSDIVIQLKEGVILGHERKEGDELSEQ 120
 Db 42 SLRYTAL-----VGODVYLCQLSPCKDAMSSD--IRWIDHRTSGFVHNYONGED--LEQ 92
 OY 121 DEMFRGTAVFAVDQVYGNASLRLKNVQLDAGTYKCYITTSKKGANLETKGAFSMP 180
 Db 93 MEYKGTETLRRLGSLSGNDLRLTAVSTSDSGSCAVLDGGYADA----- 140
 OY 181 EVNVYVASSETLRCEAPRMFPQPTVW-----ASQYDQ 215
 Db 141 --VVDLEVSPP-----FSQITHPKVVALAVITVILVGSFYITVFLRKKAETTKK 189
 OY 216 ANSEVSNTEFELNS-----ENVTKVSVLYVNTVINT--YSCMIENDIKAKAGDI-KVT 268
 Db 190 GKDAELEGMDAKIGTLAELEFRDPAKLETIVENLRNTEFAKTLASELERRNAQDLKLA 249
 OY 269 ESEIKRSHLOLNSKAS 286
 Db 250 SDLVQOTKAVAEKLSQWS 267

RESULT 7

T28137
 Ig V-region-like B-G antigen, isoform 1 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T28137
 R:Milne, S.; Kaufman, J.; Beck, S.
 Submitted to the EMBL Data Library, May 1998
 A:Description: DNA sequencing and analysis of the chicken major histocompatibility comp
 A:Reference number: Z20475
 A:Accession: T28137
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-340 <MIL>
 A:Cross-references: EMBL:AL023516; PIDN:CAA18958.1
 A:Experimental source: clone CB12
 C:Genetics:
 A:Gene: B-G 2
 A:Map position: 16
 A:Introns: 34/1; 148/1; 183/1; 190/1; 197/1; 204/1; 211/1; 218/1; 225/1; 232/1; 240/1; 2

Query Match 9.6%; Score 150.5; DB 2; Length 340;
 Best Local Similarity 32.4%; Pred. No. 0.00037;
 Matches 35; Conservative 22; Mismatches 40; Indels 11; Gaps 4;

OY 63 SITVTYVASAGNIGEDGILSCFEP--DIKLSDIVIQLKEGVILGHERKEGDELSEQ 120
 Db 42 SLRYTAL-----VGODVYLCQLSPCKDAMSSD--IRWIDHRTSGFVHNYONGED--LEQ 92
 OY 121 DEMFRGTAVFAVDQVYGNASLRLKNVQLDAGTYKCYITTSKKGANA 168
 Db 93 MEYKGTETLRRLGSLSGNDLRLTAVSTSDSGSCAVLDGGYADA 140

RESULT 8

A55717
 myelin/oligodendrocyte glycoprotein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 08-Oct-1999
 C:Accession: A55717; C47712
 R:Daubas, P.; Pham-Dinh, D.; Dautigny, A.
 Genomics 23, 36-41, 1994
 A:Title: Structure and polymorphism of the mouse myelin/oligodendrocyte glycoprotein
 A:Reference number: A55717; M0ID:95130110
 A:Accession: A55717
 A:Molecule type: DNA
 A:Residues: 1-247 <DAU>
 A:Cross-references: GB:L29498
 R:Pham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Roussel, G.; Pontarotti, P.; Roeckel,
 Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993
 A:Title: Myelin/oligodendrocyte glycoprotein is a member of a subset of the immunoglo
 A:Reference number: A47712; M0ID:93376728
 A:Accession: C47712
 A:Molecule type: mRNA
 A:Residues: 30-95, 'E', '97-247' <PHA>
 A:Cross-references: GB:L20942; M0ID:g399588; PIDN:AAA03180.1; PID:g399589
 C:Genetics:
 A:Gene: MOG
 A:Map position: 17
 A:Note: encoded within the MHC
 C:Function:
 A:Description: may be involved in lipid interaction; may be involved in cell-cell com
 C:Keywords: glycoprotein; myelin; transmembrane protein
 F:1-29/Domain: signal sequence #status predicted <Sig>
 F:30-247/Product: myelin/oligodendrocyte glycoprotein #status predicted <MAT>
 F:151-179/Domain: transmembrane #status predicted <TM>
 F:204-229/Domain: transmembrane #status predicted <TM2>
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.5%; Score 150; DB 2; Length 247;
 Best Local Similarity 23.8%; Pred. No. 0.00027;

Matches 34; Conservative 33; Mismatches 66; Indels 10; Gaps 2;

OY 37 WS-----IISIIITAGAILIIGFISGRHSITVTYVASAGNIGEDGILSCFEPDIK 90
 Db 5 WSPSPSCFSLILLL-----LLOLSCSYAQOFVIGPYIRALVGEDEALPRISPGKN 60
 OY 91 LSDIVIQLKEGVILGHERKEGDELSEQDEMFRGTAVFAVDQVYGNASLRLKNVQLT 150
 Db 61 ATGEGVWYSPSRVYVHLRNKGDQDAEPAPEYRGTELTETISGVKYLRIQNVRS 120
 OY 151 DAGTYKCYITTSKKGANLETK 173
 Db 121 DEGYTCTFFRDHSYQEEANMEIK 143

RESULT 9

A48754
 B7-2 antigen - human
 N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
 C:Species: Homo sapiens (hmn)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 10:11:58 ; Search time 12.21 Seconds

(without alignments)
509,803 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574
Sequence: 1 HASNAHGRQRQLHASTQI.....SSFAISMALLPLSPYIMLK 309

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database : Issued_Patents_AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 212.5 | 13.5 | 610 | 2 | US-08-724-394A-5 |
| 3 | 211.5 | 13.4 | 589 | 2 | US-08-724-394A-1 |
| 4 | 207.5 | 13.2 | 342 | 2 | US-08-724-394A-6 |
| 5 | 186 | 11.8 | 581 | 2 | US-08-724-394A-2 |
| 6 | 183 | 11.6 | 581 | 2 | US-08-724-394A-3 |
| 7 | 147.5 | 9.4 | 323 | 5 | PCT-US94-09642-2 |
| 8 | 147.5 | 9.4 | 329 | 2 | US-08-456-104-2 |
| 9 | 147.5 | 9.4 | 329 | 2 | US-08-101-624-2 |
| 10 | 147.5 | 9.4 | 329 | 3 | US-08-479-744A-2 |
| 11 | 147.5 | 9.4 | 329 | 4 | US-08-280-757B-2 |
| 12 | 147.5 | 9.4 | 329 | 4 | US-08-205-697A-23 |
| 13 | 147.5 | 9.4 | 329 | 4 | PCT-US95-02576-23 |
| 14 | 144 | 9.1 | 247 | 5 | PCT-US94-10257A-2 |
| 15 | 143.5 | 9.1 | 309 | 2 | US-08-456-104-4 |
| 16 | 143.5 | 9.1 | 309 | 3 | US-08-479-744A-23 |
| 17 | 143.5 | 9.1 | 309 | 4 | US-08-280-757B-23 |
| 18 | 143.5 | 9.1 | 309 | 4 | US-08-205-697A-21 |
| 19 | 143.5 | 9.1 | 309 | 5 | PCT-US95-02576-21 |
| 20 | 143.5 | 9.1 | 314 | 4 | US-08-205-697A-13 |
| 21 | 143.5 | 9.1 | 314 | 5 | PCT-US95-02576-13 |
| 22 | 132 | 8.4 | 478 | 5 | PCT-US95-08493-13 |
| 23 | 132 | 8.4 | 478 | 5 | PCT-US95-08493-15 |
| 24 | 132 | 8.4 | 868 | 1 | US-08-374-834-1 |
| 25 | 132 | 8.4 | 868 | 2 | US-08-644-271-1 |
| 26 | 132 | 8.4 | 868 | 5 | PCT-US95-08493-21 |
| 27 | 128 | 8.1 | 365 | 4 | US-08-928-383B-23 |

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|----|-------|-----|-----|---|-------------------|-------------------|
| 28 | 128 | 8.1 | 365 | 4 | US-08-928-383B-24 | Sequence 24, Appl |
| 29 | 127 | 8.1 | 946 | 5 | PCT-US95-08493-13 | Sequence 13, Appl |
| 30 | 124.5 | 7.9 | 208 | 3 | US-08-630-172-15 | Sequence 15, Appl |
| 31 | 124 | 7.9 | 306 | 2 | US-08-147-772-4 | Sequence 4, Appl |
| 32 | 124 | 7.9 | 306 | 2 | US-08-456-104-8 | Sequence 8, Appl |
| 33 | 124 | 7.9 | 306 | 2 | US-08-101-624-25 | Sequence 25, Appl |
| 34 | 124 | 7.9 | 306 | 3 | US-08-153-262-4 | Sequence 4, Appl |
| 35 | 124 | 7.9 | 306 | 3 | US-08-479-744A-31 | Sequence 31, Appl |
| 36 | 124 | 7.9 | 306 | 4 | US-08-280-757B-31 | Sequence 31, Appl |
| 37 | 124 | 7.9 | 306 | 4 | US-09-159-135-4 | Sequence 4, Appl |
| 38 | 124 | 7.9 | 306 | 4 | US-08-205-697A-17 | Sequence 17, Appl |
| 39 | 124 | 7.9 | 306 | 5 | PCT-US95-02576-17 | Sequence 17, Appl |
| 40 | 124 | 7.9 | 320 | 4 | US-08-205-697A-2 | Sequence 2, Appl |
| 41 | 124 | 7.9 | 320 | 5 | PCT-US95-02576-2 | Sequence 2, Appl |
| 42 | 123.5 | 7.8 | 869 | 1 | US-08-374-834-16 | Sequence 16, Appl |
| 43 | 123.5 | 7.8 | 869 | 2 | US-08-644-271-29 | Sequence 29, Appl |
| 44 | 123 | 7.8 | 365 | 4 | US-08-928-383B-26 | Sequence 26, Appl |
| 45 | 123 | 7.8 | 467 | 2 | US-07-916-098A-45 | Sequence 45, Appl |

ALIGNMENTS

RESULT 1
US-08-724-394A-4
; Sequence 4, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Laner, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Filts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..540
; OTHER INFORMATION: /note="BTF5"
US-08-724-394A-4

[illegible]

RESULT 4
US-08-724-394A-6
Sequence 6, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-Oct-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Filts, Renee A.
REGISTRATION NUMBER: 35,116
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEFAX: 415-576-0200
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..342
OTHER INFORMATION: /note= "BTP4"
US-08-724-394A-6

| Query Match | 13.2% | Score 207.5 | DB 2 | Length 342 |
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| Best Local Similarity | 26.1% | Pred. No. 3.4e-13 | | |
| Matches | 55 | Conservative 31 | Mismatches 94 | Indels 31 |
| | | | Gaps 5 | |
| QY | 75 | IGEDGILSCFEPDRIKLSDIVIQWLKEGYLGVHEFKESGKDELSEQDEMFGRGTAVAFDQ | 134 | |
| DB | 47 | VGEDADLPCHLEPPTMSAETMELKWSSLRQVAVYADKKEVEDRQAPYRGRTSILRGG | 106 | |
| QY | 135 | VIVGNASLRIRKNVQLTDAGTYKCYIIITSGKKNANLEYTGAF-SMPEVNV-DYNASSTP | 192 | |
| DB | 107 | ITAGGAALRIHNVTASDSCKYLCYQDGDYFKALVELVVALGSLHAEVGYEDGCIH | 166 | |
| QY | 193 | LRCEAPRPFQPTVVM-----ASQYDQGANSEVNSNTSEHLSENVTKKVSV | 240 | |
| DB | 167 | LECRSTGMVPOQIQMSNAKNGENIPAVEAPYVADQGLYEVA-----ASV | 211 | |
| QY | 241 | LYNVITNNYSCMIENDI--AKATGDIKYTE | 269 | |
| DB | 212 | IMRGSGGEVSCILRNSSLGLEKTAISISTAD | 242 | |

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RESULT      5
US-08-724-394A-2
; Sequence 2, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Laufer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..581
; OTHER INFORMATION: /note= "Brp1"
US-08-724-394A-2

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Query Match 11.8%; Score 186; DB 2; Length 581;
Best Local Similarity 23.6%; Pred. No. 1.3e-10;
Matches 52; Conservative 41; Mismatches 115; Indels 12; Gaps 5;

QY 42 IITLLAGALIIIGFISGHSITVTTVASAGNIGEDGIISCTEPEPDIKLSIDIVIMLKE 101
DB 19 LLLLLLSLCL-----VSAOFIVAGPTDPLATVAGENTTLRCHLSPEKNAEDMEVWFRS 73
QY 102 GVLGLVHEFEKDELSEODEMRGRTAVPADQVIVGNLSRLKNQOLTDAGTYKCYIIT 161
DB 74 QSPBAVFTYKGERTEQMEETRGRTTEYSKDISGSVALVHNTAENGTYRCYPOE 133
QY 162 SKKGANLANE-YKTGAFSMEPVNV-DYNASSETLRCEAPRFPQPTVWVASQVDOGA-NF 218
DB 134 GRVYDEALHLVAVAGLSKRLISMRGHEDGIRLECISSRWYKPKPLVWRDPYGVAPAL 193
QY 219 SEVSNTSFELNSENVTKVSVLYLVNTINTYSCMIENDI 258
DB 194 KEYSMP-----DADGLFMVTTAVIIRDKSVRNMSCSINTL 229

RESULT 6
US-08-724-394A-3
; Sequence 3, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Laufer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereeto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..581
; OTHER INFORMATION: /note="BTF2"
US-08-724-394A-3

Query Match 11.6%; Score 183; DB 2; Length 581;
Best Local Similarity 23.6%; Pred. No. 2.6e-10;
Matches 59; Conservative 42; Mismatches 113; Indels 36; Gaps 8;

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DB 2 EPAAALHFEPLASL-----LLLLLLLSLCLAVL-----SAGPTVGPANPLIA 45
QY 76 --GEODILSCTEPEPDIKLSIDIVIMLKEGVLVHFEKRGKDELSEODEMRGRTAVPAD 133
DB 46 WGEENTTLRCHLSPEKNAEDMEVWFRSQSPBAVFTYKGERTEQMEETRGRTTEYSKD 105
QY 134 QVIVGNASRLKNQOLTDAGTYKCYIITSKGKANLANE-YKTGAFSMEPVNV-DYNASSE 191
DB 106 DNRGSVALVHNTVAGENGITRCYFQEGRSYDEALRLVAVAGLSKPLIEKAQEDGSI 165
QY 192 TLRCAPRFPQPTVWVASQVDOGANFSEVSNTSEFL--NSENVTKVSVLYLVNTINN 248
DB 166 WLECISGVYPEPLVWRDP-----YGEVVPALKEVSIADADGLFMVTTAVIIRDKYVR 219
QY 249 TYSCTMIENDI 258
DB 220 NVCSVNNTL 229

RESULT 7
PCT-US94-09642-2
; Sequence 2, Application PC/TUS9409642
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding
; TITLE OF INVENTION: Protein and Related Reagents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation, M-3-W
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940-1000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh IIcx
; OPERATING SYSTEM: System software 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09642
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/120,606
; FILING DATE: 13-SEP-1993
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/116,882
; FILING DATE: 03-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Blasgale, John H. C.
; REGISTRATION NUMBER: 31,895
; REFERENCE/DOCKET NUMBER: DX0390K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-822-7398
; TELEFAX: 201-822-7039
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-09642-2

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APPLICANT: Mitcham, Jennifer L
APPLICANT: King, Gordon E.

3Q ID NO 415
LENGTH: 65

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file US09617747.res made by sdavld on Mon 23 Jul 101 13:49:45-PDT.

| | | |
|--------------------------------|-------------------|---------|
| Query sequence being compared: | US-09-636-801-392 | (1-309) |
| Number of sequences searched: | | 68 |
| Number of scores above cutoff: | | 68 |

Results of the initial comparison of US-09-636-801-392 (1-309) with
File : US09617747.pep

| Item | Score |
|------|-------|
| S | 34 |
| E | 69 |
| N | 103 |
| C | 137 |
| E | 172 |
| U | 206 |
| O | 240 |
| S | 275 |
| F | 309 |
| O | 341 |

| PARAMETERS | |
|-------------------------|---------|
| Similarity matrix | PAM-150 |
| Threshold level of sim. | 16% |
| Mismatch penalty | 1 |
| Gap penalty | 1.00 |
| Gap size penalty | 0.05 |
| Cutoff score | 0 |
| Randomization group | 0 |

SEARCH STATISTICS

| Scores: | Mean | Median | Standard Deviation |
|---------|-------------|--------|--------------------|
| | 18 | 11 | 37.06 |
| Times: | | | |
| | CPU | | Total Elapsed |
| | 00:00:00.00 | | 00:00:00.00 |

| | |
|--------------------------------|---|
| Number of residues: | 4 |
| Number of sequences searched: | |
| Number of scores above cutoff: | |

The scores below are sorted by initial score.

Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

| Sequence Name | Description | Int. Opt. | Length | Score | Score | Sig. | Frame |
|---------------|-------------|-----------|--------|-------|-------|------|-------|
|---------------|-------------|-----------|--------|-------|-------|------|-------|

| | | | | |
|-----------------------------------------------|-----|-----|------|---|
| 1. US-09-617-747-39 Sequence 392, Application | 309 | 309 | 7.85 | 0 |
| The list of other best scores is: | | | | |

| Sequence Name | Description | *** 7 standard deviations above mean *** | *** 1 standard deviation above mean *** | *** 0 standard deviation from mean *** | *** 1 standard deviation below mean *** | *** 7 standard deviations below mean *** | Int. Opt. | Length | Score | Stg. | Frame |
|----------------------|-------------------------------|------------------------------------------|-----------------------------------------|----------------------------------------|-----------------------------------------|------------------------------------------|-----------|--------|-------|------|-------|
| 2. US-09-617-747-39 | Sequence 393, Application 402 | 282 | 282 | 282 | 282 | 7.12 | 0 | | | | |
| 3. US-09-617-747-41 | Sequence 415, Application 403 | 65 | 65 | 65 | 65 | 1.27 | 0 | | | | |
| 4. US-09-617-747-41 | Sequence 414, Application 403 | 35 | 36 | 36 | 36 | 0.49 | 0 | | | | |
| 5. US-09-617-747-41 | Sequence 412, Application 403 | 35 | 35 | 35 | 35 | 0.46 | 0 | | | | |
| 6. US-09-617-747-40 | Sequence 402, Application 403 | 21 | 22 | 22 | 22 | 0.11 | 0 | | | | |
| 7. US-09-617-747-41 | Sequence 412, Application 403 | 20 | 21 | 21 | 21 | 0.08 | 0 | | | | |
| 8. US-09-617-747-41 | Sequence 411, Application 403 | 20 | 21 | 21 | 21 | 0.08 | 0 | | | | |
| 9. US-09-617-747-39 | Sequence 395, Application 403 | 20 | 21 | 21 | 21 | 0.08 | 0 | | | | |
| 10. US-09-617-747-39 | Sequence 399, Application 403 | 20 | 21 | 21 | 21 | 0.08 | 0 | | | | |
| 11. US-09-617-747-39 | Sequence 398, Application 403 | 20 | 21 | 21 | 21 | 0.08 | 0 | | | | |
| 12. US-09-617-747-41 | Sequence 410, Application 403 | 20 | 20 | 20 | 20 | 0.05 | 0 | | | | |
| 13. US-09-617-747-40 | Sequence 401, Application 403 | 20 | 20 | 20 | 20 | 0.05 | 0 | | | | |
| 14. US-09-617-747-40 | Sequence 401, Application 403 | 20 | 20 | 20 | 20 | 0.05 | 0 | | | | |
| 15. US-09-617-747-40 | Sequence 400, Application 403 | 20 | 20 | 20 | 20 | 0.05 | 0 | | | | |
| 16. US-09-617-747-39 | Sequence 397, Application 403 | 20 | 20 | 20 | 20 | 0.05 | 0 | | | | |
| 17. US-09-617-747-39 | Sequence 395, Application 403 | 20 | 20 | 20 | 20 | 0.05 | 0 | | | | |
| 18. US-09-617-747-39 | Sequence 394, Application 403 | 20 | 20 | 20 | 20 | 0.05 | 0 | | | | |
| 19. US-09-617-747-40 | Sequence 408, Application 403 | 20 | 19 | 19 | 19 | 0.03 | 0 | | | | |
| 20. US-09-617-747-40 | Sequence 409, Application 403 | 20 | 19 | 19 | 19 | 0.03 | 0 | | | | |
| 21. US-09-617-747-40 | Sequence 407, Application 403 | 20 | 19 | 19 | 19 | 0.03 | 0 | | | | |
| 22. US-09-617-747-40 | Sequence 406, Application 403 | 20 | 19 | 19 | 19 | 0.03 | 0 | | | | |
| 23. US-09-617-747-40 | Sequence 404, Application 403 | 20 | 19 | 19 | 19 | 0.03 | 0 | | | | |
| 24. US-09-617-747-39 | Sequence 396, Application 403 | 20 | 19 | 19 | 19 | 0.03 | 0 | | | | |
| 25. US-09-617-747-43 | Sequence 431, Application 428 | 10 | 11 | 11 | 11 | -0.19 | 0 | | | | |
| 26. US-09-617-747-42 | Sequence 425, Application 428 | 10 | 11 | 11 | 11 | -0.19 | 0 | | | | |
| 27. US-09-617-747-42 | Sequence 422, Application 428 | 10 | 11 | 11 | 11 | -0.19 | 0 | | | | |
| 28. US-09-617-747-42 | Sequence 422, Application 428 | 10 | 11 | 11 | 11 | -0.19 | 0 | | | | |
| 29. US-09-617-747-43 | Sequence 430, Application 428 | 9 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 30. US-09-617-747-43 | Sequence 429, Application 428 | 9 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 31. US-09-617-747-44 | Sequence 442, Application 442 | 9 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 32. US-09-617-747-44 | Sequence 442, Application 442 | 9 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 33. US-09-617-747-43 | Sequence 435, Application 435 | 10 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 34. US-09-617-747-43 | Sequence 434, Application 435 | 10 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 35. US-09-617-747-43 | Sequence 433, Application 435 | 10 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 36. US-09-617-747-43 | Sequence 432, Application 435 | 10 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 37. US-09-617-747-43 | Sequence 430, Application 435 | 10 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 38. US-09-617-747-43 | Sequence 429, Application 435 | 10 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 39. US-09-617-747-42 | Sequence 427, Application 427 | 10 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 40. US-09-617-747-42 | Sequence 426, Application 427 | 10 | 10 | 10 | 10 | -0.22 | 0 | | | | |
| 41. US-0 | | | | | | | | | | | |

Sequence 412, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 412

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 21 Optimized Score = 21 Significance = 0.08
Residue Identity = 100% Matches = 20 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

240 250 260 270 280 290 300 X
VLXVNTINNTSCMIENDIAKATGDIKVTSEIKRSHQLLNSKASLCVSEFAISWALLPLSPYLMK
|||||
SSFAISWALLPLSPYLMK
X
10 20

8. US-09-636-801-392 (1-309)
US-09-617-747-41 Sequence 411, Application US/09617747

Sequence 411, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 411

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 21 Optimized Score = 21 Significance = 0.08
Residue Identity = 100% Matches = 20 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

240 250 260 270 280 290 300 X
VTMKVSVLYVNTINNTSCMIENDIAKATGDIKVTSEIKRSHQLLNSKASLCVSEFAISWALLPLSP
|||||
SKASLCVSEFAISWALLPL
X
10 20

YLMK

9. US-09-636-801-392 (1-309)
US-09-617-747-40 Sequence 405, Application US/09617747

Sequence 405, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 405

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 21 Optimized Score = 21 Significance = 0.08
Residue Identity = 100% Matches = 20 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

150 160 170 180 190 200 210 X
RLKNQLDAGTKYKCIITISKGNANLEKTKGATSMPEVNDYNASSETLRCGAPRRFPPTVYMASOYD
|||||
LRCGAPRRFPPTVYMASOY
X
10 20

220 230 240 250 260
GANFSEVNTSEFELNSENVTMKVSVLYVNTINNTSCMIENDIAKAT

10. US-09-636-801-392 (1-309)
US-09-617-747-39 Sequence 399, Application US/09617747

Sequence 399, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 399

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

Initial Score = 21 Optimized Score = 21 Significance = 0.08
Residue Identity = 100% Matches = 20 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

60 70 80 90 100 110 120 X
IIGFISGRHSITVTVASAGNIGEDGILCTFEPDILSDIVYQMLKEGVGLVHERKEKDELSEDEMF
|||||
VLGLVHERKEKDELSEDEMF
X
10 20

130 140 150 160 170
RGRTAVFADQVIVGNASLRKNNVQLTDAGTYKCYITITSKGNANLEY

TYPE: PRT
ORGANISM: Homo sapiens

Initial Score - 65 Optimized Score - 65 Significance - 1.27
Residue Identity - 100% Matches - 65 Mismatches - 0
Gaps - 0 Conservative Substitutions - 0

120 130 140 150 160 170 180
GKDELSEODEMFRGRTAVFADQVIVGNASLRKKNVLTDAAGTYKCYITTSKGGNANLEKYGAFSPMEVNV
|||||
X
KGGNANLEKYGAFSPMEVNV
X
10 20

190 200 210 220 230 240 250
DYASSETLRCEAPRMFPPTVYMASOVDOGANFSEVNTSMKVVSVLYNTINNTYSCHMEN
|||||
DYASSETLRCEAPRMFPPTVYMASOVDOGANFSEVNTSFE
30 40 50 60 X

260 270
DIATKATGDIKVFTESEIKRRSH

4. US-09-636-801-392 (1-309)
US-09-617-747-41 Sequence 414, Application US/09617747

Sequence 414, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 414
LENGTH: 35
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score - 36 Optimized Score - 36 Significance - 0.49
Residue Identity - 100% Matches - 35 Mismatches - 0
Gaps - 0 Conservative Substitutions - 0

60 70 80 90 100 X 110 120
IIGFGISGRHSITVTVASAGNIGEDGILSCFPEPDIKLSDIVIOMLKEGVGLVHFEKKGDELSEODEMF
|||||
VGLGVHFEKKGDELSEODEMF
X
10 20

130 140 150 160 170 180
RGRTAVFADQVIVGNASLRKKNVLTDAAGTYKCYITTSKGGNANLEKYGAFSPMEVNV
|||||
RGRTAVFADQVIV
30 X

5. US-09-636-801-392 (1-309)
US-09-617-747-41 Sequence 413, Application US/09617747

Sequence 413, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 413
LENGTH: 35
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score - 35 Optimized Score - 35 Significance - 0.46
Residue Identity - 100% Matches - 35 Mismatches - 0
Gaps - 0 Conservative Substitutions - 0

10 20 30 40 50 60 70
GGRQLHSASTQIRWERSPAMASIGQILFWISITITITLAGATALLIGFGISGRHSITVTVASAGNIGEDG
|||||
ISGRHSITVTVASAGNIGEDG
X
10 20

80 90 X 100 110 120 130 140
ILSCFPEPDIKLSDIVIOMLKEGVGLVHFEKKGDELSEODEMFRGRTAVFADQVIVGNASL
|||||
ILSCFPEPDIKLS
30 X

6. US-09-636-801-392 (1-309)
US-09-617-747-40 Sequence 402, Application US/09617747

Sequence 402, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 402
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score - 22 Optimized Score - 22 Significance - 0.11
Residue Identity - 100% Matches - 21 Mismatches - 0
Gaps - 0 Conservative Substitutions - 0

100 110 120 130 140 150 160 X
QMLKEGVGLVHFEKKGDELSEODEMFRGRTAVFADQVIVGNASLRKKNVLTDAAGTYKCYITTSKGGN
|||||
VQLTDAAGTYKCYITTSKGN
X
10 20

170 180 190 200 210
NLEKYGAFSPMEVNVNDYNASSETLRCEAPRMFPPTVYMASOVDOGAN

7. US-09-636-801-392 (1-309)
US-09-617-747-41 Sequence 412, Application US/09617747

160 170 180 190 200
X 10 20
YKCYITTSKGNANLEFKTGAFSMPEVAVDYNASSETLRCEAPRPF

15. US-09-636-801-392 (1-309)
US-09-617-747-40 Sequence 400, Application US/09617747

Sequence 400, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 400
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 20 Optimized Score = 20 Significance = 0.05
Residue Identity = 100% Matches = 20 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

70 80 90 100 110 120 130 X
TVASAGNIGEDGILSCFEPDIKLSDIVIOMKEGVLGVHEFKGKDELSDQEMFRGRTAVFADQVIVGN
|||||
SPQDEMFRGRTAVFADQVIV
X 10 20

140 150 160 170 180
ASLRLLKNVOLTDAFTYKCYITTSKGNANLEFKTGAFSMPEVAVDYN

16. US-09-636-801-392 (1-309)
US-09-617-747-39 Sequence 397, Application US/09617747

Sequence 397, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 397
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 20 Optimized Score = 20 Significance = 0.05
Residue Identity = 100% Matches = 20 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

30 40 50 60 70 X 80 90 X

EPSPAMASIGQILFWISIIIIILAGALAILIGFISGRHSITVTVASAGNIGEDGILSCFEPDIKLSDI
|||||
GNIGEDGILSCFEPDIKLS
X 10 20

17. US-09-636-801-392 (1-309)
US-09-617-747-39 Sequence 395, Application US/09617747

Sequence 395, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 395
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 20 Optimized Score = 20 Significance = 0.05
Residue Identity = 100% Matches = 20 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 X 50 60 X 70
HASASAGRQROHSAHQVIRWEPSPAMASIGQILFWISIIIIILAGALAILIGFISGRHSITVTVASAG
|||||
IIILAGALAILIGFISGRH
X 10 20

80 90 100 110
GNIGEDGILSCFEPDIKLSDIVIOMKEGVLGVHEFK

18. US-09-636-801-392 (1-309)
US-09-617-747-39 Sequence 394, Application US/09617747

Sequence 394, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 394
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 20 Optimized Score = 20 Significance = 0.05
Residue Identity = 100% Matches = 20 Mismatches = 0

11. US-09-636-801-392 (1-309)
US-09-617-747-39 Sequence 398, Application US/09617747

Sequence 398, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 398
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|----|--------------|---|------|
| Initial Score | - | 21 | Optimized Score | - | 21 | Significance | - | 0.08 |
| Residue Identity | - | 100% | Matches | - | 20 | Mismatches | - | 0 |
| Gaps | - | 0 | Conservative Substitutions | - | 0 | | - | 0 |

40 50 60 70 80 90 100 X
SISIIILAGAILIIGFISGRHSITVTVASAGNIGEDGILCTFEEDPIKISDIYIOWLKEGVLGLVHE
|||||
DIXLSDIYIOWLKEGVLGLV
X 10 20

110 120 130 140 150
EKEGDELSEDEMRGRGTAVFAFADQVIYGNASLRKKNVQLTDAGTYKC
12. US-09-636-801-392 (1-309)
US-09-617-747-41 Sequence 410, Application US/09617747

Sequence 410, Application US/09617747
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 410
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|----|--------------|---|------|
| Initial Score | - | 20 | Optimized Score | - | 20 | Significance | - | 0.05 |
| Residue Identity | - | 100% | Matches | - | 20 | Mismatches | - | 0 |
| Gaps | - | 0 | Conservative Substitutions | - | 0 | | - | 0 |

220 230 240 250 260 270 280 X
FSEVSNISFELNSENVTKVYVLYNTINTYSCMIENDAKATGDIKVESIKRRSHQLLNKSKSLV
|||||
TESIKRRSHQLLNKSKSL
X 10 20

SSFFAISWALLPLSPYMLK

13. US-09-636-801-392 (1-309)
US-09-617-747-40 Sequence 403, Application US/09617747

Sequence 403, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 403
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|----|--------------|---|------|
| Initial Score | - | 20 | Optimized Score | - | 20 | Significance | - | 0.05 |
| Residue Identity | - | 100% | Matches | - | 20 | Mismatches | - | 0 |
| Gaps | - | 0 | Conservative Substitutions | - | 0 | | - | 0 |

120 130 140 150 160 170 180 X
GKDELSEDEMRGRGTAVFAFADQVIYGNASLRKKNVQLTDAGTYKCIITTSKGNANLEYRTGAFSPMEVAV
|||||
KGGKANLEYRTGAFSPMEV
X 10 20

14. US-09-636-801-392 (1-309)
US-09-617-747-40 Sequence 401, Application US/09617747

Sequence 401, Application US/09617747
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 401
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|----|--------------|---|------|
| Initial Score | - | 20 | Optimized Score | - | 20 | Significance | - | 0.05 |
| Residue Identity | - | 100% | Matches | - | 20 | Mismatches | - | 0 |
| Gaps | - | 0 | Conservative Substitutions | - | 0 | | - | 0 |

90 100 110 120 130 140 150 X
CTFEPDIKISDIYIOWLKEGVLGVHEKEGDELSEDEMRGRGTAVFAFADQVIYGNASLRKKNVQLTDAGT
|||||
DQVIYGNASLRKKNVQLTDA

LENGTH: 20
TYPE: PRF
ORGANISM: Homo sapiens

Initial Score = 19 Optimized Score = 19 Significance = 0.03
Residue Identity = 100% Matches = 20 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

160 170 180 190 200 210 220 X
YIITSKGNANLEKTKGAFSMPEVNDVYNSSETLRCEAPRFQPIYVNASQVDGANSFSEVNTSELN
|||||
WASQVDGANSFSEVNTSEFE
X
10

230 240 250 260 270
SENVTMKVSVLYNTINTNTSCMIENDIARATGDIKTESEIKRRSH

23. US-09-636-801-392 (1-309)
US-09-617-747-40 Sequence 404, Application US/09617747

Sequence 404, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 404
LENGTH: 20
TYPE: PRF
ORGANISM: Homo sapiens

Initial Score = 19 Optimized Score = 19 Significance = 0.03
Residue Identity = 100% Matches = 20 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

130 140 150 160 170 180 190 X
TAVFADQYIVGNASLRKKNVOLTDACTYKCYIITSKGNANLEKTKGAFSMPEVNDVYNSSETLRCEAPR
|||||
SMPEVNDVYNSSETLRCEA
X
10

200 210 220 230 240
WFPQTVVWASQVDGANSFSEVNTSEFEINSENVTKVSVLYNTIN

24. US-09-636-801-392 (1-309)
US-09-617-747-39 Sequence 396, Application US/09617747

Sequence 396, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 396
LENGTH: 20
TYPE: PRF
ORGANISM: Homo sapiens

Initial Score = 19 Optimized Score = 19 Significance = 0.03
Residue Identity = 100% Matches = 20 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70 X
GROROLHSASTQIRWEPSPAMASLGQLFWISITSIILAGAILIGFGISGRSITVTYVNASGNIGEDG
|||||
ISGRSITVTYVNASGNIG
X
10

80 90 100 110 120
ILSCFEPDIKLSDIVIQWLKRGVGLVHEFEGKDELSEQDEMRGR

25. US-09-636-801-392 (1-309)
US-09-617-747-43 Sequence 431, Application US/09617747

Sequence 431, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 431
LENGTH: 10
TYPE: PRF
ORGANISM: Homo sapiens

Initial Score = 11 Optimized Score = 11 Significance = -0.19
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

50 60 70 80 90 100 X
GAILIIGFGISGRSITVTYVNASGNIGEDGILSCFEPDIKLSDIVIQWLKRGVGLVHEFEGKDELSE
|||||
WLKRGVGLV
X
10

120 130 140 150
ODEMRGRRTAVFADQYIVGNASLRKKNVOLTDACTYK

26. US-09-636-801-392 (1-309)
US-09-617-747-42 Sequence 428, Application US/09617747

Sequence 428, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

Gaps - 0 Conservative Substitutions - 0

10 20 30 40 50 60 70
HASAHSGRQLHSASTQIRWEPSPAMSLGQILFWSTIIIIIIAGALALLIGRISGRHSITVTVASA
|||||
MASLQILFWSTIIIIIIA
X 10 20

80 90
GNIGEDGILSCFEPPIKLSDIYIO

19. US-09-636-801-392 (1-309)
US-09-617-747-40 Sequence 409, Application US/09617747

Sequence 409, Application US/09617747

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 409
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score - 19 Optimized Score - 19 Significance - 0.03
Residue Identity - 100% Matches - 20 Mismatches - 0
Gaps - 0 Conservative Substitutions - 0

210 220 230 240 250 X 260 270 X
QPTVVASQVDGANSFSEVNTSEFELNSENVTMKVSVLYNTINNYSMIENDAKATGDIKVTSEIKR
|||||
MIENDAKATGDIKVTSEI
X 10 20

280 290 300
RSHQLLNKASLCVSSFPAISWALLPLSPYMLK

20. US-09-636-801-392 (1-309)
US-09-617-747-40 Sequence 408, Application US/09617747

Sequence 408, Application US/09617747

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 408
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score - 19 Optimized Score - 19 Significance - 0.03
Residue Identity - 100% Matches - 20 Mismatches - 0
Gaps - 0 Conservative Substitutions - 0

190 200 210 220 230 240 250 X
ASSETLRCEAPRWFPPQPTVVASQVDGANSFSEVNTSEFELNSENVTMKVSVLYNTINNYSMIENDIA
|||||
VSVLYNTINNYSMIEND
X 10 20

260 270 280 290 300
KATGDIKVTSEIKRSHQLLNKASLCVSSFPAISWALLPLSPYMLK

21. US-09-636-801-392 (1-309)
US-09-617-747-40 Sequence 407, Application US/09617747

Sequence 407, Application US/09617747

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 407
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score - 19 Optimized Score - 19 Significance - 0.03
Residue Identity - 100% Matches - 20 Mismatches - 0
Gaps - 0 Conservative Substitutions - 0

180 190 200 210 220 X 230 240 X
KTGFMSPEVNVDMASSFELRCCEAPRWFPPQPTVVASQVDGANSFSEVNTSEFELNSENVTMKVSVLYNV
|||||
NTSEFELNSENVTMKVSVLY
X 10 20

250 260 270 280 290
TINNYSMIENDAKATGDIKVTSEIKRSHQLLNKASLCVSSF

22. US-09-636-801-392 (1-309)
US-09-617-747-40 Sequence 406, Application US/09617747

Sequence 406, Application US/09617747

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 406

LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

50 60 70 80 90 100 X 110
ILAAIALIIGFISGRHSITVTYASAGNIGEDGILSCFPEPIKLSDIYIOMLKGVGLGVHFEKGEKDE
|||||
VIOMLKGV
X

120 130 140 150
LSEDEMRGRTAVFADQVIYGNASLRKNVQLTDAG

31. US-09-636-801-392 (1-309)
US-09-617-747-44 Sequence 447, Application US/09617747

Sequence 447, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 447

LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

250 260 270 280 290 300 X
TYSCEMIENDIAKATGDIKYTESIKRSHLQLNSKASLCVSSFFAISWALLPLSPYLMLK
|||||
LLPLSPYL
X

32. US-09-636-801-392 (1-309)
US-09-617-747-44 Sequence 442, Application US/09617747

Sequence 442, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 442

LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

50 60 70 80 90 100 X 110
GAILLIIGFISGRHSITVTYASAGNIGEDGILSCFPEPIKLSDIYIOMLKGVGLGVHFEKGEKDE
|||||
WLKGVGL
X

120 130 140 150
ODEMRGRTAVFADQVIYGNASLRKNVQLTDAGTYK

33. US-09-636-801-392 (1-309)
US-09-617-747-43 Sequence 436, Application US/09617747

Sequence 436, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 436

LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

250 260 270 280 290 300 X
NTYSCMIENDIAKATGDIKYTESIKRSHLQLNSKASLCVSSFFAISWALLPLSPYLMLK
|||||
ALLPLSPYL
X

34. US-09-636-801-392 (1-309)
US-09-617-747-43 Sequence 435, Application US/09617747

Sequence 435, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 435

FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617.747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 428

LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|----|--------------|---|-------|
| Initial Score | = | 11 | Optimized Score | = | 11 | Significance | = | -0.19 |
| Residue Identity | = | 100% | Matches | = | 10 | Mismatches | = | 0 |
| Gaps | = | 0 | Conservative Substitutions | = | 0 | | | 0 |

250 260 270 280 290 300 X
NTYSCMIENDIAKATGDIKVTSEIKRSHLQLNKSKSLCVSFFAISMALLPLSPYLMK
|||||
ALLPLSPYLM
X 10

27. US-09-636-801-392 (1-309)

US-09-617-747-42 Sequence 425, Application US/09617747

Sequence 425, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617.747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 425
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|----|--------------|---|-------|
| Initial Score | = | 11 | Optimized Score | = | 11 | Significance | = | -0.19 |
| Residue Identity | = | 100% | Matches | = | 10 | Mismatches | = | 0 |
| Gaps | = | 0 | Conservative Substitutions | = | 0 | | | 0 |

250 260 270 280 290 300 X
NNTYSCMIENDIAKATGDIKVTSEIKRSHLQLNKSKSLCVSFFAISMALLPLSPYLMK
|||||
WALLPLSPYL
X 10

28. US-09-636-801-392 (1-309)

US-09-617-747-42 Sequence 422, Application US/09617747

Sequence 422, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617.747
CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 422
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|----|--------------|---|-------|
| Initial Score | = | 11 | Optimized Score | = | 11 | Significance | = | -0.19 |
| Residue Identity | = | 100% | Matches | = | 10 | Mismatches | = | 0 |
| Gaps | = | 0 | Conservative Substitutions | = | 0 | | | 0 |

250 260 270 280 290 300 X
TYSCMIENDIAKATGDIKVTSEIKRSHLQLNKSKSLCVSFFAISMALLPLSPYLMK
|||||
LLPLSPYLM
X 10

29. US-09-636-801-392 (1-309)

US-09-617-747-45 Sequence 450, Application US/09617747

Sequence 450, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617.747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 450
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|----|--------------|---|-------|
| Initial Score | = | 10 | Optimized Score | = | 10 | Significance | = | -0.22 |
| Residue Identity | = | 100% | Matches | = | 9 | Mismatches | = | 0 |
| Gaps | = | 0 | Conservative Substitutions | = | 0 | | | 0 |

250 260 270 280 290 300 X
VTNNTYSCMIENDIAKATGDIKVTSEIKRSHLQLNKSKSLCVSFFAISMALLPLSPYLMK
|||||
ATSMALLPL
X

30. US-09-636-801-392 (1-309)

US-09-617-747-44 Sequence 449, Application US/09617747

Sequence 449, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617.747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 449

FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 430

LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

30 40 50 60 70 80 90 100
SLGGLFWSTIIIIIIAGALALIGICGRHSITVTYVASAGNIGEDICSTCEPPIKLSDIYIOWLKE
|||||
IIISCTPEPDI
X
10

110 120 130
GVLGIVHFEKGEKDELSEQDEMFGRGTAIVFADQYIVGN

39. US-09-636-801-392 (1-309)
US-09-617-747-42 Sequence 429, Application US/09617747

Sequence 429, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 429

LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

230 240 250 260 270 280 290 300
NSENVTKVSVLYNTINNTYSCMIENDIAKATGDIKYESEIKRSHLOLNKRSALCVSSEFAISWALL
|||||
OLNKSASLIC
X
10

PLSPYLMK

40. US-09-636-801-392 (1-309)
US-09-617-747-42 Sequence 427, Application US/09617747

Sequence 427, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 427

LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

100 110 120 130 140 150
WLKEGVLGIVHFEKGEKDELSEQDEMFGRGTAIVFADQYIVGNASRLKNVOLTDAQTYKCYITISKGNAN
|||||
OITDAGTYKC
X
10

170 180 190 200
LEYKTGAFSPMEPVNDYNASSETLRCEAPRMPQPPTV

41. US-09-636-801-392 (1-309)
US-09-617-747-42 Sequence 426, Application US/09617747

Sequence 426, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 426

LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70
HASAHASGRQRLHSASTIQRWEPSPAMSLGQILFWSTIIIIIIAGALALIGICGRHSITVTYVASA
|||||
IIIIAGALAL
X
10

80 90 100
GNIGEGIIISCTPEPPIKLSDIYIOWLKEGV

42. US-09-636-801-392 (1-309)
US-09-617-747-42 Sequence 424, Application US/09617747

Sequence 424, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.

LENGTH: 10
TYPE: PR
ORGANISM: Homo sapiens
Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
40 50 60 70 80 90 100
LEWSTIIIIIIAGAILIIGFGISGRHSITVTYVASAGNIGDEGIIISCTFEPPDIKLSDIYQWLKEGVGL
IIIIIIIIII
FEPPDIKLSDI
X
10

110 120 130 140
VHEFEKGDELSEQDEMERGRTRAVPADQYIVGNASLRL

35. US-09-636-801-392 (1-309)
US-09-617-747-43 Sequence 434, Application US/09617747

Sequence 434, Application US/09617747
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 434
LENGTH: 10
TYPE: PR
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
10 20 30 40 50 60 70
SGHROLHSASTOIRNEPSPAMASLGQILFWSIIIIIIIIAGAILIIGFGISGRHSITVTYVASAGNIGED
IIIIIIIIII
GISGRHSITV
X
10

80 90 100 110
GILSCFEPPDIKLSDIYQWLKEGVGLVHEFEKGDE

36. US-09-636-801-392 (1-309)
US-09-617-747-43 Sequence 433, Application US/09617747

Sequence 433, Application US/09617747
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 433
LENGTH: 10
TYPE: PR
ORGANISM: Homo sapiens
Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
10 20 30 40 50 60 70
HASAHASGROROLHSASTOIRNEPSPAMASLGQILFWSIIIIIIIIAGAILIIGFGISGRHSITVTYVASA
IIIIIIIIII
QILEWSTISI
X
10

80 90
GNIGEDGILSCFEPPDIKLS

37. US-09-636-801-392 (1-309)
US-09-617-747-43 Sequence 432, Application US/09617747

Sequence 432, Application US/09617747
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 432
LENGTH: 10
TYPE: PR
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
230 240 250 260 270 280
LNSENVTKYVSVLNVNTINNYSCMIENDAKATGDIKYTESEIKRRSHLOLNSKASLCVSSFFAISWAL
IIIIIIIIII
LOLLNSKASL
X
10

300
LPLSPYMLK

38. US-09-636-801-392 (1-309)
US-09-617-747-43 Sequence 430, Application US/09617747

Sequence 430, Application US/09617747
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

Sequence 418, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 418
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
230 240 250 260 270 280 X 300
SENTMKVSVLYVNTINNTSCMIENDIARATGDIKYESEIKRRSHLQLNSKASLCVSSFFAISMALLP
|||||
LNSKASLCV
X
10

LSPYLMLK

47. US-09-636-801-392 (1-309)
US-09-617-747-41 Sequence 417, Application US/09617747

Sequence 417, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 417
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
10 20 30 X 50 60 70
HASAHASRQQLHASTQITWEPSPAMASIGQILFWSIISIIIIILAGALAILIGFISGRHSITVTYVASA
|||||
SIGQILFWSI
X
10

80
GNIGEDGILCTFEPDI

48. US-09-636-801-392 (1-309)
US-09-617-747-41 Sequence 416, Application US/09617747

Sequence 416, Application US/09617747
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 416
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
40 50 60 70 80 90 X 110
ISIIIIAGALAILIGFISGRHSITVTYVASAGNIGEDGILCTFEPDIKSLDIVIQLKEGVGLVHEPK
|||||
KLSLDIVIQL
X
10

120 130 140
EGKDELSQDEMFRCRTAVFADOVTVGNASRLKNVOL

49. US-09-636-801-392 (1-309)
US-09-617-747-39 Sequence 390, Application US/09617747

Sequence 390, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 390
LENGTH: 438
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 51 Significance = -0.22
Residue Identity = 20% Matches = 22 Mismatches = 58
Gaps = 21 Conservative Substitutions = 9

EDALNQLFRNSISYSDCOVSTPRSRVPHRHHTGVDSLCSFSLARRVDAIYEELFRMTNGTOLQNTT
290 300 310 320 330 X 340 350
HASAHA-----SGRQRO---
|||||

APPLICANT: Fling, Steven P.
 APPLICANT: Retter, Marc W.
 APPLICANT: Fangner, Gary Richard
 APPLICANT: Reed, Steven G.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.462C3
 CURRENT APPLICATION NUMBER: US/09/617,747
 CURRENT FILING DATE: 2000-07-17
 NUMBER OF SEQ ID NOS: 455
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 424
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
 Residue Identity = 100% Matches = 10 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

130 140 150 160 170 180 190
 MGRGRTAVADQYIVGNASLRKNVQLTGATYKCYITISKGKGNANLEKYGAFSPMEVNDYNASSETLR
 ||||||||
 KTGFASMEVY
 X 10

200 210 220 230
 CEAPRRFPQPTVYMASQVDOGANFSEVNTSELNSEN

43. US-09-636-801-392 (1-309)
 US-09-617-747-42 Sequence 423, Application US/09617747

Sequence 423, Application US/09617747
 GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
 APPLICANT: King, Gordon E.
 APPLICANT: Algate, Paul A.
 APPLICANT: Fling, Steven P.
 APPLICANT: Retter, Marc W.
 APPLICANT: Fangner, Gary Richard
 APPLICANT: Reed, Steven G.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.462C3
 CURRENT APPLICATION NUMBER: US/09/617,747
 CURRENT FILING DATE: 2000-07-17
 NUMBER OF SEQ ID NOS: 455
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 423
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
 Residue Identity = 100% Matches = 10 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

210 220 230 240 250 X 270
 PPTVYMASQVDOGANFSEVNTSELNSENVTMKVSVLYNVTINNYSCTMIENDIAKATGDIKYTESEIK
 ||||||||
 CMIENDIAKA
 X 10

280 290 300
 RRSHTQLNSKASLCVSSFPAISWALLPLSPYMLK

44. US-09-636-801-392 (1-309)
 US-09-617-747-42 Sequence 421, Application US/09617747
 GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
 APPLICANT: King, Gordon E.
 APPLICANT: Algate, Paul A.
 APPLICANT: Fling, Steven P.
 APPLICANT: Retter, Marc W.
 APPLICANT: Fangner, Gary Richard
 APPLICANT: Reed, Steven G.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.462C3
 CURRENT APPLICATION NUMBER: US/09/617,747
 CURRENT FILING DATE: 2000-07-17
 NUMBER OF SEQ ID NOS: 455
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 421
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
 Residue Identity = 100% Matches = 10 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70
 HASAHSGRORLSASTQIRWEPSPAMASLGQILFWSITISITIIILAGATILIGFGISGRHSITVTYVASA
 ||||||||
 ILFWSITISII
 X 10

80 90
 GNIGEDGILSCFREPDIKLSLD

45. US-09-636-801-392 (1-309)
 US-09-617-747-41 Sequence 419, Application US/09617747

Sequence 419, Application US/09617747
 GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
 APPLICANT: King, Gordon E.
 APPLICANT: Algate, Paul A.
 APPLICANT: Fling, Steven P.
 APPLICANT: Retter, Marc W.
 APPLICANT: Fangner, Gary Richard
 APPLICANT: Reed, Steven G.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.462C3
 CURRENT APPLICATION NUMBER: US/09/617,747
 CURRENT FILING DATE: 2000-07-17
 NUMBER OF SEQ ID NOS: 455
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 419
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo sapiens

Initial Score = 10 Optimized Score = 10 Significance = -0.22
 Residue Identity = 100% Matches = 10 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

240 250 260 270 280 290 300
 KVSVALYNVTINNTYSCTMIENDIAKATGDIKYTESEIKRRSHQLNSKASLCVSSFPAISWALLPLSPYML
 ||||||||
 SLCVSSFPAI
 X 10

46. US-09-636-801-392 (1-309)
 US-09-617-747-41 Sequence 418, Application US/09617747
 LK

US-09-617-747-45 Sequence 454, Application US/09617747

Sequence 454, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 454
LENGTH: 9
TYPE: prt
ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

90 100 110 120 130 140 150
EPDIKSDIYQWLKEGYLVHFEKSGKDELSDDEMFGRGTAVFADQVVGNSLRKNVQLTDAGTYKC
|||||
IVGNASLRL
X X X

160 170 180 190
YIITSKGGNANLEYKTGARSMEPVNDYNASSETLR

54. US-09-636-801-392 (1-309)
US-09-617-747-45 Sequence 453, Application US/09617747

Sequence 453, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 453
LENGTH: 9
TYPE: prt
ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

40 50 60 70 80 90 100
QILFWSIISIIILAGAILIIGFISGRHSITVTVASAGNIGEDGILSTFEPDIKSDIYQWLKEGYL
|||||
CTFEPDIKL
X X X

110 120 130 140
GLVHFEKSGKDELSDDEMFGRGTAVFADQVVGNS

55. US-09-636-801-392 (1-309)
US-09-617-747-45 Sequence 452, Application US/09617747

Sequence 452, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 452
LENGTH: 9
TYPE: prt
ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70
HASAHASGRQRLHSASTQIMWERSPMASLGLFWSIISIIILAGAILIIGFISGRHSITVTTVASA
|||||
IALIIGFGI
X X X

80 90 100
GNIGEDGILSTFEPDIKSDIYQWLKEGYLVH

56. US-09-636-801-392 (1-309)
US-09-617-747-45 Sequence 451, Application US/09617747

Sequence 451, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 451
LENGTH: 9
TYPE: prt
ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70
HASAHASGRQRLHSASTQIMWERSPMASLGLFWSIISIIILAGAILIIGFISGRHSITVTTVASA
|||||
SLGOLFWS
X X X

53. US-09-636-801-392 (1-309)

190 200 210 220 230 X 240 250
VNVYDMSSEFLRCEAPRWFPPQPTVYMASQVQGANFSEVNTSELSNVTMAYSVLNTNTNTSCM
|||||||
NVTMKVSV
X

260 270 280 290
IENDIAKATGDIKVTSESEIKRRSHQLNLSKASLCVS

61. US-09-636-801-392 (1-309)
US-09-617-747-44 Sequence 443, Application US/09617747

Sequence 443, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 443

LENGTH: 9

TYPE: PRF

ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 X 50 X 60 70
HASAHASGRQLHSASTQIMWSPAMASIGQLFWISIIILLAGAIIILIFGISGRHSITVTYVASA
|||||||
ILAGAIIL
X

80 90 100
GNIGEDGILSCTFEPDILSDIVIQWLKEG

62. US-09-636-801-392 (1-309)
US-09-617-747-44 Sequence 441, Application US/09617747

Sequence 441, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 441

LENGTH: 9

TYPE: PRF

ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 X 50 X 60 70
HASAHASGRQLHSASTQIMWSPAMASIGQLFWISIIILLAGAIIILIFGISGRHSITVTYVASA
|||||||
ILAGAIIL
X

80 90 100
GNIGEDGILSCTFEPDILSDIVIQWLKEG

63. US-09-636-801-392 (1-309)
US-09-617-747-44 Sequence 440, Application US/09617747

Sequence 440, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 440

LENGTH: 9

TYPE: PRF

ORGANISM: Homo sapiens

Initial Score = 9 Optimized Score = 9 Significance = -0.24
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

190 200 210 220 230 X 240 X 250
YNASSETLRCEAPRWFPPQPTVYMASQVQGANFSEVNTSELSNVTMAYSVLNTNTNTSCMIEND
|||||||
KVSVLYTV
X

260 270 280 290
IAKATGDIKVTSESEIKRRSHQLNLSKASLCVSSFFA

64. US-09-636-801-392 (1-309)
US-09-617-747-43 Sequence 439, Application US/09617747

Sequence 439, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

APPLICANT: Fling, Steven P.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary Richard

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.462C3

CURRENT APPLICATION NUMBER: US/09/617,747

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 439

LENGTH: 9

80
GNIGEDGILSCFEPD

57. US-09-636-801-392 (1-309)
US-09-617-747-44 Sequence 448, Application US/09617747

Sequence 448, Application US/09617747

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Flinn, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 448
LENGTH: 9

TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|---|--------------|---|-------|
| Initial Score | - | 9 | Optimized Score | - | 9 | Significance | - | -0.24 |
| Residue Identity | - | 100% | Matches | - | 9 | Mismatches | - | 0 |
| Gaps | - | 0 | Conservative Substitutions | - | 9 | | - | 0 |

230 240 250 260 270 280 290 300
 SENWTKVSVLVNTYNTYSCMIENDIAKATGDIKTESEIKRRSHQLNLSKASLCVSSFFALSWALLP
 |||||
 LNLSKASLC
 X X X

LSPLYMLK

58. US-09-636-801-392 (1-309)
US-09-617-747-44 Sequence 446, Application US/09617747

Sequence 446, Application US/09617747

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Flinn, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 446
LENGTH: 9

TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|---|--------------|---|-------|
| Initial Score | - | 9 | Optimized Score | - | 9 | Significance | - | -0.24 |
| Residue Identity | - | 100% | Matches | - | 9 | Mismatches | - | 0 |
| Gaps | - | 0 | Conservative Substitutions | - | 9 | | - | 0 |

80 90 100 110 120 130 140 150
 GLSCFEPDILSDIVIQMLKEGVGLVHERKEGDELSEODEMRGRTAVFADQVIYGNASLRKNQVLT

160 170 180
 DAQYKCYIITSKGNANLEKKTGAFSMPEVNVN
 |||||
 AVFADQVIV
 X X

59. US-09-636-801-392 (1-309)
US-09-617-747-44 Sequence 445, Application US/09617747

Sequence 445, Application US/09617747

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Flinn, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 445
LENGTH: 9

TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|---|--------------|---|-------|
| Initial Score | - | 9 | Optimized Score | - | 9 | Significance | - | -0.24 |
| Residue Identity | - | 100% | Matches | - | 9 | Mismatches | - | 0 |
| Gaps | - | 0 | Conservative Substitutions | - | 9 | | - | 0 |

80 90 100 110 120 X 130 140
 AGNIGEDGILSCFEPDILSDIVIQMLKEGVGLVHERKEGDELSEODEMRGRTAVFADQVIYGNASLR
 |||||
 EMFRGRTAV
 X X

150 160 170 180
 LKNVQLDAGTYKCYIITSKGNANLEKKTGAFSM

60. US-09-636-801-392 (1-309)
US-09-617-747-44 Sequence 444, Application US/09617747

Sequence 444, Application US/09617747

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Flinn, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 444
LENGTH: 9

TYPE: PRT
ORGANISM: Homo sapiens

| | | | | | | | | |
|------------------|---|------|----------------------------|---|---|--------------|---|-------|
| Initial Score | - | 9 | Optimized Score | - | 9 | Significance | - | -0.24 |
| Residue Identity | - | 100% | Matches | - | 9 | Mismatches | - | 0 |
| Gaps | - | 0 | Conservative Substitutions | - | 9 | | - | 0 |

TYPE: PRT
ORGANISM: Homo sapiens

Initial Score - 9 Optimized Score - 9 Significance - -0.24
Residue Identity - 100% Matches - 9 Mismatches - 0
Gaps - 0 Conservative Substitutions - 0

230 240 250 260 270 280 290 300
NSENTMKVSVLYNTINTNTYSCHIENDIAKATGDIKYTESEIKRRSHQLNLNSKASLCVSSFFAISWALL
|||||
QLNKSASL
X X

PLSPYLMLK

65. US-09-636-801-392 (1-309)
US-09-617-747-43 Sequence 438, Application US/09617747

Sequence 438, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 438
LENGTH: 9

TYPE: PRT
ORGANISM: Homo sapiens

Initial Score - 9 Optimized Score - 9 Significance - -0.24
Residue Identity - 100% Matches - 9 Mismatches - 0
Gaps - 0 Conservative Substitutions - 0

HASAHASGRQLHSASTQIRWPSPMASISQLLEWSTISITIIILAGAILIGIGISGRHSITVTVASA
|||||
ILFWSITSI
X X

80 90
GNIGEDGILSTCFEPDIKLS

66. US-09-636-801-392 (1-309)
US-09-617-747-43 Sequence 437, Application US/09617747

Sequence 437, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 437
LENGTH: 9

TYPE: PRT
ORGANISM: Homo sapiens

Initial Score - 9 Optimized Score - 9 Significance - -0.24
Residue Identity - 100% Matches - 9 Mismatches - 0
Gaps - 0 Conservative Substitutions - 0

240 250 260 270 280 290 300
KVSVLYNTINTNTYSCHIENDIAKATGDIKYTESEIKRRSHQLNLNSKASLCVSSFFAISWALLPLSPYLK
|||||
SLCVSSFFA
X X

LK

67. US-09-636-801-392 (1-309)
US-09-617-747-42 Sequence 420, Application US/09617747

Sequence 420, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3
CURRENT APPLICATION NUMBER: US/09/617,747
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 420
LENGTH: 10

TYPE: PRT
ORGANISM: Homo sapiens

Initial Score - 9 Optimized Score - 9 Significance - -0.24
Residue Identity - 100% Matches - 10 Mismatches - 0
Gaps - 0 Conservative Substitutions - 0

190 200 210 220 230 240 250 260
SETLRCEAPRWFPQPTVWASQVDOGANSFSEVSNISFELNSENVTKVSVLYNTINTNTYSCHIENDIAKA
|||||
VLNVNTINT
X 10

270 280 290
TGDIKYTESEIKRRSHQLNLNSKASLCVSSFFAISWALL

68. US-09-636-801-392 (1-309)
US-09-617-747-38 Sequence 388, Application US/09617747

Sequence 388, Application US/09617747
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C3

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> 0 <
0110 Intelligenetics
> 0 <

FastDB : Fast Pairwise Comparison of Sequences
Release 5.4

Results file US09404879.res made by sdavid on Mon 23 Jul 101 13:41:48-PDT.

Query sequence being compared: US-09-636-801-392 (1-309)
Number of sequences searched: 6
Number of scores above cutoff: 6

Results of the initial comparison of US-09-636-801-392 (1-309) with:
File : US09404879A.pep

100-
N 50-
U 50-
M 50-
B 50-
E 50-
R 50-
O 10-
F 10-
S 10-
U 5-
Q 5-
D 5-
E 5-
N 5-
C 5-
S 5-
SCORE 0 34 69 103 137 172 206 240 275 309
STDDEV 0 1 1 1 1 1 1 1 1 1

PARAMETERS
Similarity matrix PAM-150
Threshold level of sim. 16%
Mismatch penalty 1
Gap penalty 1.00
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

SEARCH STATISTICS
Scores: Mean Median Standard Deviation
104 11 148.07
Times: CPU Total Elapsed
00:00:00.00 00:00:00.00

Number of residues: 3548
Number of sequences searched: 6
Number of scores above cutoff: 6

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was found:

Sequence Name Description Init. Opt. Length Score Score Sig. Frame

1. US-09-404-879A-3 Sequence 392, Application 309 309 309 1.38 0
The list of other best scores is:

| Sequence Name | Description | Length | Score | Score | Score | Sig. | Frame |
|---------------------------------------------------|-------------------------------------------|--------|-------|-------|-------|------|-------|
| 2. US-09-404-879A-3 Sequence 393, Application 282 | **** 1 standard deviation above mean **** | 282 | 282 | 282 | 1.20 | 0 | |
| 3. US-09-404-879A-3 Sequence 390, Application 438 | **** 0 standard deviation from mean **** | 438 | 10 | 51 | -0.63 | 0 | |
| 4. US-09-404-879A-3 Sequence 389, Application 833 | | 833 | 10 | 51 | -0.63 | 0 | |
| 5. US-09-404-879A-3 Sequence 312, Application 914 | | 914 | 10 | 51 | -0.63 | 0 | |
| 6. US-09-404-879A-3 Sequence 388, Application 772 | | 772 | 7 | 153 | -0.66 | 0 | |

1. US-09-636-801-392 (1-309)
US-09-404-879A-3 Sequence 392, Application US/09404879A

Sequence 392, Application US/09404879A
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 392
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens

Initial Score = 309 Optimized Score = 309 Significance = 1.38
Residue Identity = 100% Matches = 309 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
HASAHSGRORLHASASTOIRWEPSPAMASLGILFWSTISIIILAGATALLIGISGRHSITVTYVASA
HASAHSGRORLHASASTOIRWEPSPAMASLGILFWSTISIIILAGATALLIGISGRHSITVTYVASA
X 10 20 30 40 50 60 70
GNIGEDGILSCFEPDILKISDIYIOWLKEGYLGVHFEKGRKDELSBQDEMFRGRTAVFADQYIVGNASIRL
GNIGEDGILSCFEPDILKISDIYIOWLKEGYLGVHFEKGRKDELSBQDEMFRGRTAVFADQYIVGNASIRL
X 80 90 100 110 120 130 140
KNQOLPDAGTYKCYIITTSKSGNANLEFKTGAFAPEVNVNDYNAASSTLRCEAPRFPPTTYVMAOYDGA
KNQOLPDAGTYKCYIITTSKSGNANLEFKTGAFAPEVNVNDYNAASSTLRCEAPRFPPTTYVMAOYDGA
X 150 160 170 180 190 200 210
NFESEVNTSFELNSENVTKVSVLYNVITINNTYSCHIENDIKAKGDIYVTSSEIKRSHLOLLNSKASLC
NFESEVNTSFELNSENVTKVSVLYNVITINNTYSCHIENDIKAKGDIYVTSSEIKRSHLOLLNSKASLC
X 220 230 240 250 260 270 280
VSSFFAISWALPLPLSPYMLK
VSSFFAISWALPLPLSPYMLK
X 290 300
VSSFFAISWALPLPLSPYMLK
VSSFFAISWALPLPLSPYMLK
X 290 300

2. US-09-636-801-392 (1-309)

US-09-404-879A-3 Sequence 393, Application US/09404879A

Sequence 393, Application US/09404879A
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.462C2

CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 393

LENGTH: 282

TYPE: PRP

ORGANISM: Homo sapiens

Initial Score - 282 Optimized Score - 282 Significance - 1.20

Residue Identity - 100% Matches - 282 Mismatches - 0

Gaps - 0 Conservative Substitutions - 0

HASAHASGRHQLHSASTQIRWEPSPAMASLGQILFWSITISIIIIAGALALIGFGISGRHSITVTYASA

|||||

MASLGQILFWSITISIIIIAGALALIGFGISGRHSITVTYASA

X

10 20 30 40 50 60 70

80 90 100 110 120 130 140

GNIGDGLISCFEPDILSDIVOMLKEGVGLVHEFREGKDELSEODEMRGRTAVFADQVIYGNASLRL

|||||

GNIGDGLISCFEPDILSDIVOMLKEGVGLVHEFREGKDELSEODEMRGRTAVFADQVIYGNASLRL

50 60 70 80 90 100 110

120 130 140 150 160 170 180

KNQVLDTAGTCYITTSKGNANLMEKTFGAFSPMEVVDVNASSETLRCAAPRFPPOPTVYMASOVDGA

|||||

KNQVLDTAGTCYITTSKGNANLMEKTFGAFSPMEVVDVNASSETLRCAAPRFPPOPTVYMASOVDGA

220 230 240 250 260 270 280

NESEVSNFSFELNSENVTMKVSVLYNTYNTSCMIENDIAKATGDIKTESIKRSHQLLNKASLRL

|||||

NESEVSNFSFELNSENVTMKVSVLYNTYNTSCMIENDIAKATGDIKTESIKRSHQLLNKASLRL

190 200 210 220 230 240 250 260

VSSFFAISMALPLSPYLMLK

|||||

VSSFFAISMALPLSPYLMLK

270 280 X

3. US-09-636-801-392 (1-309)

US-09-404-879A-3 Sequence 390, Application US/09404879A

Sequence 390, Application US/09404879A
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.462C2

CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 390

LENGTH: 438

TYPE: PRP

ORGANISM: Homo sapiens

Initial Score - 10 Optimized Score - 51 Significance - -0.63

Residue Identity - 20% Matches - 22 Mismatches - 58

Gaps - 21 Conservative Substitutions - 9

EDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVDSLCNFSPLARRVDRAVAIYEFLRMTNGTOLQNF

220 300 310 320 330 340 350

20 30 40 50 60 70 80

LHSASTQIR---WEPSPAMASLGQILFWSITISIIIIAGALALIGFGISGRHSITVTYASAGNIGEDGIL

|||||

LDRSSVLVDGYFPNRNEPLTGNSDLPFMAV--ILIGLAGLGLITCL-ICG---VLVYTRRRKKEGEYVVOQ

360 370 380 390 400 410 420

90 100 110 120 130 140

SCT--FEEDIKLSDIVOMLKEGVGLVHEFREGKDELSEODEMRGRTAVFADQVIYGNASLRLK

|||||

OCPGYOSHLDLEDLQ

430 X

4. US-09-636-801-392 (1-309)

US-09-404-879A-3 Sequence 389, Application US/09404879A

Sequence 389, Application US/09404879A
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.462C2

CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 389

LENGTH: 833

TYPE: PRP

ORGANISM: Homo sapiens

Initial Score - 10 Optimized Score - 51 Significance - -0.63

Residue Identity - 20% Matches - 22 Mismatches - 58

Gaps - 21 Conservative Substitutions - 9

EDALNQLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVDSLCNFSPLARRVDRAVAIYEFLRMTNGTOLQNF

680 690 700 710 720 730 740 750

20 30 40 50 60 70 80

LHSASTQIR---WEPSPAMASLGQILFWSITISIIIIAGALALIGFGISGRHSITVTYASAGNIGEDGIL

|||||

LDRSSVLVDGYFPNRNEPLTGNSDLPFMAV--ILIGLAGLGLITCL-ICG---VLVYTRRRKKEGEYVVOQ

760 770 780 790 800 810

90 100 110 120 130 140

SCT--FEEDIKLSDIVOMLKEGVGLVHEFREGKDELSEODEMRGRTAVFADQVIYGNASLRLK

|||||

OCPGYOSHLDLEDLQ

820 830 X

5. US-09-636-801-392 (1-309)

US-09-404-879A-3 Sequence 312, Application US/09404879A

Sequence 312, Application US/09404879A
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

```

APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 312
LENGTH: 914
TYPE: PRT
ORGANISM: Homo sapien

Initial Score = 10 Optimized Score = 51 Significance = -0.63
Residue Identity = 20% Matches = 22 Mismatches = 58
Gaps = 21 Conservative Substitutions = 9

```

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```

Db 19 LCLIALAG---LHSSSGIS-----QVTK-----SVKEMALISCOTNINISDELAMRIYW 65
Qy 99 LKEG---VLGLVHEFEKDELSODEMERGRVAFADQYIVGNASIRLKNVOLDAGTYK 156
Db 66 QKQDQMWISII---SGQVEWPE---YKNRT--PPD--IINNLSMLIALNLSKQTYT 114
Qy 157 CYITTSKRGKGNANLEYKGA-----FSMPEV---NVDYASSETLRCAPRNFPPT 205
Db 115 C-VVQKNNGSEFRRHRLTSVLTSLIRADFPVPSITDIGHDPDV--KRIRCSASGGFPEPR 171
Qy 206 VYMASQVQGANFSEVSNMSEFELNSENTMKVSVL-VNVTINNYSOCMIENDIAKAGD 264
Db 172 LAM---MEDGEELNAV-VITYDQDLDTELYSVSELDENVNHNHSIVCLIK-----YGE 221
Qy 265 IKVTE-----SEIKRRSHQLNLNSKASLCVSPFAISMALLPLSPYLM 308
Db 222 LSVSGIFPMWKRQPEPIDQLP-----FWYIIPVSGALVL 256

RESULT 5
MOG_RAT 5
ID MOG_RAT STANDARD: PRT: 245 AA.
AC 063345:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.
GN MOG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
[1]
RN RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93085763; PubMed=1453482;
RA Gardiner M.V., Amiguet P., Linington C., Mathieu J.-M.;
RT "Myelin/oligodendrocyte glycoprotein is a unique member of the
RT immunoglobulin superfamily."
RL J. Neurosci. Res. 33:177-187(1992).
RN [2]
RP SEQUENCE OF 28-245 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93376728; PubMed=8367453;
RA Pham-Dinh D., Matteil M.-G., Nussbaum J.-L., Rousset G.,
RA Portarotti P., Roedel N., Mather I.H., Artzt K., Lindahl K.F.,
RA Dautigny A.;
RT "Myelin/oligodendrocyte glycoprotein is a member of a subset of the
RT immunoglobulin superfamily encoded within the major
RT histocompatibility complex."
RL Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
RN [3]
RP STRUCTURE BY NMR OF 62-82.
RX MEDLINE=97354172; PubMed=9210466;
RA Alouf-Abo S., Wilson J.C., Bernard C.C.A., von Izstein M.;
RT "A confocal study of the human and rat cephalic myelin
RT oligodendrocyte glycoprotein peptides 35-55."
RL Eur. J. Biochem. 246:59-70(1997).
CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
CC COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
CC CELL COMMUNICATION.
CC -1- SUBUNIT: MAY FORM HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
CC LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
CC MEMBRANES.
CC -1- DEVELOPMENTAL STAGE: A PEAK OF EXPRESSION HAS BEEN OBSERVED
CC BETWEEN POSTNATAL DAYS 15 AND 25, COINCIDENT WITH THE PERIOD OF
CC ACTIVE MYELINATION.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE DOMAIN. BELONGS TO THE RTN/MOG SUBFAMILY.
CC -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)
CC WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).

```

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CC -----
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CC -----
CC DR EMBL; M99485; AAA41628.1;
CC DR EMBL; L21995; AAF74786.1;
CC DR InterPro: IPR003006;
CC DR Pfam; PF00047; 1g; 1.
CC KW Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
CC FT SIGNAL 1 27
CC FT CHAIN 28 245 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
CC FT DOMAIN 28 155 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 156 176 POTENTIAL.
CC FT DOMAIN 177 208 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 209 229 POTENTIAL.
CC FT DOMAIN 230 245 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 44 132 IG-LIKE V-TYPE DOMAIN.
CC FT DISULFD 51 125 POTENTIAL.
CC FT CARBOHD 58 58 N-LINKED (GLCNAc. ...) (POTENTIAL).
CC SQ SEQUENCE 245 AA; 27881 MW; C97F8AD60D6A32B4 CRC64;

Query Match 9.7%; Score 152; DB 1; Length 245;
Best Local Similarity 26.2%; Pred. No. 2e-05; Mismatches 55; Indels 24; Gaps 5;
Matches 39; Conservative 31;

Qy 37 WS-----IISIIIL-----AGAILIIGISGRHSITVTVASAGNIGEDSLCT 84
Db 5 WLSLSPCLSLTLILQLSRSYAGQFR-VIGPG-----HPIRL-----VQDEALPCR 52

Qy 85 FEPDLKLSIVQLKEGVLGVHEFEKDELSODEMERGRVAFADQYIVGNASIRL 144
Db 53 ISPGNAGMEGWYRSPFSRVHLRYRNGKDDADAEAPRETLKESIGEGKVALRI 112

Qy 145 KVVOLTDAQTYKCYITTSKGNANLEYK 173
Db 113 QVNRSEDEGTYCFRRDHSYQEEAAVELK 141

RESULT 6
MOG_MOUSE 6
ID MOG_MOUSE STANDARD: PRT: 246 AA.
AC 061885; Q62003; F70364;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.
GN MOG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=95130110; PubMed=7829100;
RA Daubas P., Pham-Dinh D., Dautigny A.;
RT "Structure and polymorphism of the mouse myelin/oligodendrocyte
RT glycoprotein gene."
RL Genomics 23:36-41(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX Gardiner M.V., Mathieu J.M.;
RA "Murine and human MOG are highly conserved: cDNA analysis."
RL Trans. Am. Soc. Neurochem. 24:234-234(1993).
RN [3]
RP SEQUENCE OF 29-246 FROM N.A.
RC STRAIN=BAUB/C; TISSUE=Brain;

```

RX MEDLINE=93376728; PubMed=8367453;
 RA Pham-Dinh D., Mattei M.-G., Nusbaum J.-L., Rousset G.,
 RA Pontarotti P., Roeckel N., Mather I.H., Attizt K., Lindahl K.F.,
 RA Dautigny A.;
 RT "Myelin/Oligodendrocyte glycoprotein is a member of a subset of the
 RT immunoglobulin superfamily encoded within the major
 RT histocompatibility complex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
 RN [4]
 RP SEQUENCE OF 29-54.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RA MEDLINE=92218912; PubMed=1373175;
 RA Amiguet P., Gardiner M.V., Zanetta J.-P., Mathieu J.-M.;
 RT "Purification and partial structural and functional characterization
 RT of mouse myelin/oligodendrocyte glycoprotein.";
 RL J. Neurochem. 58:1676-1682(1992).
 CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
 CC COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
 CC CELL COMMUNICATION.
 CC -1- SUBUNIT: MAY FORM HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
 CC LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
 CC MEMBRANES.
 CC -1- DISEASE: REDUCED CONCENTRATIONS OF MOG ARE OBSERVED IN JIMPY AND
 CC QUACKING DYSMYELINATING MUTANT MICE.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.
 CC -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)
 CC WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
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 CC -----
 DR EMBL: L29503; AAC42023.1; -;
 DR EMBL: L29498; AAC42023.1; JOINED.
 DR EMBL: L29500; AAC42023.1; JOINED.
 DR EMBL: L29501; AAC42023.1; JOINED.
 DR EMBL: L29499; AAC42023.1; JOINED.
 DR EMBL: L29502; AAC42023.1; JOINED.
 DR EMBL: U64572; AAB08096.1; -;
 DR EMBL: L20942; AAA03180.1; -;
 DR MGD: MGI:97435; M09.
 DR InterPro: IPR003006; -;
 DR Pfam: PF00047; 1g; 1.
 KW Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
 FT CHAIN 1 28
 FT DOMAIN 29 246 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
 FT TRANSMEM 157 177 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 178 209 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 210 230 POTENTIAL.
 FT DOMAIN 231 246 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 45 133 IG-LIKE V-TYPE DOMAIN.
 FT DISULFID 52 126 POTENTIAL.
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 21 21 L -> L (IN REF. 2).
 FT CONFLICT 32 32 R -> G (IN REF. 4).
 FT CONFLICT 35 95 G -> E (IN REF. 3).
 FT CONFLICT 169 169 P -> S (IN REF. 2).
 SQ SEQUENCE 246 AA; 28271 MW; 1F1A8AAAD5CF889 CRC64;

Query Match 9.6%; Score 150.5; DB 1; Length 246;
 Best Local Similarity 23.8%; Pred. No. 2.7e-05;
 Matches 34; Conservative 33; Mismatches 65; Indels 11; Gaps 2;
 QY 37 WS-----IISIIIIAGALALIIGFISGRHSITVTVAASAGNIGDGLSCFFEDIK 90

Db 5 WSFSPSCFSLSLLL-----LQLSCTYACOFRIYICGYPIRALYGDABLPCHISCKN 59
 QY 91 LSDIVIMLKEGVGLVHERKEGKDELSEDEMERTAVPADOVIVGNLSRLKNOVLT 150
 Db 60 ATGMEVGMSPFSRVRVHLVRNGKDQDAEAPREYGRTELLKETSISGKVTLRIONRFS 119
 QY 151 DACTYKCIYITTSKGNANLEYK 173
 Db 120 DEGGYTCFPRDHSYQEBAMELK 142
 RESULT 7
 ID CD86_HUMAN STANDARD; PRT; 329 AA.
 AC P42081; Q13655;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2
 DE ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.2) (B70) (FUN-1) (B063).
 GN CD86 OR CD28LG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94053735; PubMed=7694363;
 RA Freeman G.J., Gribben J.G., Boussetios V.A., Ng J.W.,
 RA Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;
 RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
 RT cell proliferation.";
 RL Science 262:909-911(1993).
 RN [2]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX MEDLINE=94050123; PubMed=7694153;
 RA Akama M., Ito D., Yagita K., Okumura K., Phillips J.H.,
 RA Lanier L.L., Somoza C.;
 RT "B70 antigen is a second ligand for CTLA-4 and CD28.";
 RL Nature 366:76-79(1993).
 RN [3]
 RP SEQUENCE OF 7-329 FROM N.A.
 RC TISSUE=foreskin;
 RX MEDLINE=95331831; PubMed=7541777;
 RA Jellis C.L., Wang S.S., Rennert P., Borriello F., Sharpe A.H.,
 RA Green N.R., Gray G.S.;
 RT "Genomic organization of the gene coding for the costimulatory human
 RT B-1 lymphocyte antigen B7-2 (CD86)."
 RL Immunogenetics 42:85-89(1995).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=95088403; PubMed=7527824;
 RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
 RA Okumura K., Ito D., Akama M.;
 RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
 RT cell proliferation, cytokine production, and generation of CTL.";
 RL J. Immunol. 154:97-105(1995).
 RN [5]
 RP IDENTIFICATION AS CD86.
 RX MEDLINE=94348060; PubMed=7520767;
 RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,
 RA Nadler L.M., Wakasa H., Tedder T.F.;
 RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and
 RT activated B lymphocytes is the CD86 differentiation antigen.";
 RL Blood 84:1402-1407(1994).
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND MONOCYTES.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.

CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD86 entry: <http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm>.

CC -----

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CC -----

DR EMBL; L25259; AAA8389.1; -

DR EMBL; U04343; AAB03814.1; -

DR EMBL; U17722; AAA86473.1; -

DR EMBL; U17717; AAA86473.1; JOINED.

DR EMBL; U17718; AAA86473.1; JOINED.

DR EMBL; U17719; AAA86473.1; JOINED.

DR EMBL; U17721; AAA86473.1; JOINED.

DR MIM; 601020; -

DR InterPro: IPR000495; -

DR PROSITE; PS00290; IG_MHC; FALSE_NEG.

KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane; Receptor.

FT SIGNAL 1 23

FT CHAIN 24 329

FT DOMAIN 24 247

FT TRANSMEM 248 268

FT DOMAIN 269 329

FT DOMAIN 33 117

FT DOMAIN 149 225

FT DISULFED 157 218

FT CARBOHYD 33 33

FT CARBOHYD 47 47

FT CARBOHYD 135 135

FT CARBOHYD 146 146

FT CARBOHYD 154 154

FT CARBOHYD 177 177

FT CARBOHYD 192 192

FT CARBOHYD 213 213

FT CONFLICT 27 27

FT SEQUENCE 329 AA; 37696 MW; 65D4E3826889CFTD CRC64;

Query Match 9.48; Score 147.5; DB 1; Length 329;

Best Local Similarity 23.48; Pred. No. 7e-05;

Matches 67; Conservative 43; Mismatches 109; Indels 67; Gaps 13;

QY 50 IALLIGFSGHRSITVTVAAGNIGEDGILCTF--EPDKLSDIYOMLKEGVGLV 107

DB 12 ILFVAFILSGAIPKIAAY-----FNETADLPFCFANSQNSLSLVEFMODQENL-VL 65

QY 108 HEKKGKDELSEQDEMFGRTAFVADQYIVGNASLRKLVOLDAGTYKCYITTSKGG- 166

DB 66 NEVLGKKEKFSVHSKYGKRTSFSD-----SWTLRLNLHLQIKDKGLVCQIHHKKPTGM 120

QY 167 ----NANLEYKGA-FSMPEV-----NDYMASSEFLRCEAPFMFPQPIYVMA5QVDQGAN 217

DB 121 IRIHOMNSELVLANF5QPEIVPISITENYI-NLTCSIHGYDEP----- 166

QY 218 FSEVNTSFELSENVTAKV-----SVLKNVTI-----NNTVSCMIEN 256

DB 167 ----KKMSVLRTKSTIEYDQIMKSDQNTVELDVSSISVSFDPDYSNNTITCILET 222

QY 257 DIAKATGDIKYTESEIKR--RSHLOLNS--KASLCVSSFFAISM 297

DB 223 DKTRLLSPFSTIELEDPPRPDHPIMVITAVLPTVITICWVFLILM 268

RESULT 8

CD86_RABIT

ID CD86_RABIT STANDARD: PRI: 330 AA.

AC P42071;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE B LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2 ANTIGEN).

GN CD86.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=B/J X CHB:HM;

RX MEDLINE=95369849; PubMed=7642234;

RA Isono T., Seto A.;

RT "Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecules.";

RL Immunogenetics 42:217-220(1995).

CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE C2-LIKE AND ONE V-LIKE DOMAINS.

CC -----

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CC -----

DR EMBL; D49842; BAA08642.1; -

DR InterPro: IPR000495; -

DR PROSITE; PS00290; IG_MHC; 1.

KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane; Receptor.

FT SIGNAL 1 22

FT CHAIN 23 330

FT DOMAIN 23 247

FT TRANSMEM 248 268

FT DOMAIN 269 330

FT DOMAIN 33 117

FT DOMAIN 149 225

FT DISULFED 157 218

FT CARBOHYD 33 33

FT CARBOHYD 47 47

FT CARBOHYD 135 135

FT CARBOHYD 146 146

FT CARBOHYD 154 154

FT CARBOHYD 177 177

FT CARBOHYD 192 192

FT CARBOHYD 198 198

FT CARBOHYD 213 213

FT SEQUENCE 330 AA; 37142 MW; 935CD65C57E3EE1 CRC64;

Query Match 9.48; Score 147.5; DB 1; Length 330;

Best Local Similarity 24.08; Pred. No. 7.1e-05;

Matches 59; Conservative 44; Mismatches 80; Indels 63; Gaps 11;

QY 38 STSIITIIAGAILIGSGHSITVTVAAGNIGEDGILCTF--EPDKLSDIY 95

DB 12 TVFVALLISGASLRT-----QATNKRTADLPFCQFTNSQSRSLSELY 54

| Accession | Protein Name | Length | Source | Notes |
|-----------|--------------------------------------------------------------------------------------------------------------------------|--------|--------|----------------------------------------------------------------------|
| RA | Albous-Abd.S., Wilson J.C., Bernard C.C.A., von Itzstein M.: | | | "A conformational study of the human and rat encephalitogenic myelin |
| RT | oligodendrocyte glycoprotein peptides 35-55." | | | |
| RL | Eur. J. Biochem. 246:59-70(1997). | | | |
| CC | -1 FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN | | | |
| CC | COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL- | | | |
| CC | CELL COMMUNICATION. | | | |
| CC | -1 SUBUNIT: MAY FORM HOMO- OR HETERODIMERS BETWEEN THE DIFFERENT | | | |
| CC | ISOFORMS. | | | |
| CC | -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (ISOFORMS ALPHA-1 | | | |
| CC | AND BETA-1); TYPE I MEMBRANE PROTEIN (OTHER ISOFORMS) (POTENTIAL). | | | |
| CC | -1 ALTERNATIVE PRODUCTS: AT LEAST 9 ISOFORMS: ALPHA-1 (SHOWN HERE), | | | |
| CC | -2, -3, -4, BETA-1, -2, -3, -4 AND A SHORT ISOFORM ARE PRODUCED BY | | | |
| CC | ALTERNATIVE SPLICING. THE SHORT ISOFORM IS NOT FUNCTIONALLY | | | |
| CC | ACTIVE, IT MAY BE EXPRESSED AT LOW LEVEL IN THE ADULT. | | | |
| CC | -1 TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS | | | |
| CC | LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC | | | |
| CC | MEMBRANES. | | | |
| CC | -1 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS | | | |
| CC | ONE V-LIKE DOMAIN. BELONGS TO THE ERM/MOG SUPERFAMILY. | | | |
| CC | -1 CAUTION: DO NOT CONFUSE MYELIN OLIGODENDROCYTE GLYCOPROTEIN (MOG) | | | |
| CC | WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG). | | | |
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| CC | or send an email to license@isb-sib.ch). | | | |
| CC | ----- | | | |
| DR | EMBL: X74511; CAA52617.1; - | | | |
| DR | EMBL: Z48051; CAA88109.1; - | | | |
| DR | EMBL: U18840; AAC50361.1; - | | | |
| DR | EMBL: U18843; AAC50362.1; - | | | |
| DR | EMBL: U18798; AAC50876.1; - | | | |
| DR | EMBL: U18799; AAC50877.1; - | | | |
| DR | EMBL: U18800; AAB36870.1; - | | | |
| DR | EMBL: U18801; AAC50878.1; - | | | |
| DR | EMBL: U18803; AAC50879.1; - | | | |
| DR | EMBL: U64564; AAB08088.1; - | | | |
| DR | EMBL: U64565; AAB08089.1; - | | | |
| DR | EMBL: U64567; AAB08091.1; - | | | |
| DR | EMBL: U64568; AAB08092.1; - | | | |
| DR | EMBL: U64569; AAB08093.1; - | | | |
| DR | EMBL: U64570; AAB08094.1; - | | | |
| DR | EMBL: U64571; AAB08095.1; - | | | |
| DR | HSSP: O13740; IKTG. | | | |
| DR | MIM: 159465; - | | | |
| DR | InterPro: IPR003006; - | | | |
| DR | Pfam: PF000047; 1g.1. | | | |
| KW | Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal; | | | |
| KW | Alternative splicing. | | | |
| FT | SIGNAL | 1 | 29 | |
| FT | CHAIN | 30 | 247 | POTENTIAL. |
| FT | DOMAIN | 30 | 154 | MYELIN-OLIGODENDROCYTE GLYCOPROTEIN. |
| FT | TRANSSEM | 155 | 175 | EXTRACELLULAR (POTENTIAL). |
| FT | DOMAIN | 176 | 210 | POTENTIAL. |
| FT | TRANSEM | 211 | 231 | CYTOPLASMIC (POTENTIAL). |
| FT | DOMAIN | 232 | 247 | EXTRACELLULAR (POTENTIAL). |
| FT | DOMAIN | 46 | 134 | IG-LIKE V-TYPE DOMAIN. |
| FT | DISULF | 53 | 127 | POTENTIAL. |
| FT | CARBOHYD | 60 | 60 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | VARSPLIC | 30 | 145 | MISSING (IN ISOFORM ALPHA-4). |
| FT | VARSPLIC | 198 | 203 | DPHRLR -> GKPRHV (IN SHORT ISOFORM). |
| FT | VARSPLIC | 204 | 247 | MISSING (IN SHORT ISOFORM). |
| FT | VARSPLIC | 198 | 236 | DPHELRYPCMKITLLEVTIVYGLPLVALITICNWLHRLA |
| FT | VARSPLIC | | | -> ESFGLVQVKEPKRT (IN ISOFORM ALPHA-3 |
| FT | VARSPLIC | | | AND ISOFORM BETA-3). |
| FT | VARSPLIC | | | MISSING (IN ISOFORM ALPHA-2 AND ISOFORM |
| FT | VARSPLIC | | | BETA-2). |
| FT | VARSPLIC | | | MISSING (IN ISOFORM BETA-4). |
| FT | VARSPLIC | 198 | 243 | |

| | | | | |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------|-------------------------|-------------------------------------------------------------------------------------------------|
| | VARSPLIC | 244 | 247 | RNPE -> LPHLEALSG (IN ISOFORM BETA-1, ISOFORM BETA-2, ISOFORM BETA-3 AND ISOFORM BETA-4). |
| FT FT | CONFLICT | 171 | 171 | v -> l (in REF. 3). |
| SO SEQUENCE | 247 AA; | 28179 MM; | 84760LFE5997ABOC CRC64; | |
| | Query Match | 9.1%; | Score 144; | DB 1; |
| | Best Local Similarity | 20.8%; | Pred. NO. | 9.1e-05; |
| | Matches 49; | Conservative 39; | Mismatches 85; | Indels 68; |
| | Gaps | | | |
| OY | 28 MASGLQIFWMSITSIHIL-----AGALLIIGFGISGRHSITYTVASACNGIED 78 | : : : | : | : : : |
| Dd | 1 NASLSRPSLPSCSLCSEFLLLILLQVSSSVAQGPRV-----TGRHPRLA-----VGDE 48 | : | : | : |
| OY | 79 GILSTFFEDPDLSDIVLIOWLKEGVLGHEKEKDELSEDENFERGTAFADQVIYG 138 | : : : : | : : : : | : : : : |
| Dd | 49 VELPCRPISPKGNATGMGWYRRPRSRYVVHLVRKGKDQCDDGAPEXRGTELLKCALIGGS 108 | : | : | : |
| OY | 139 NASHLRKNVOLTDACTGYTKCYITSKGGKANILEYTGAFSMEPVANDVASSETLERCAP 198 | : : : : | : : : : | : : : : |
| Dd | 109 KWTLLIRNRFRFDSGEGETCFEFDHSHYOEBAAE-----LVKVEDP 147 | : | : | : |
| OY | 199 RMFPQPTVMASGVDOGANFSEVSMTSPELNSENTMKRVSY-LYNVTINTNYSCM 253 | : : : : | : : : : | : : : : |
| Dd | 148 FYWSRFQUL-----VLAVALPYLLLQIIYGLVFLLCL 178 | : | : | : |
| RESULT 11 | | | | |
| ID CD86_MOUSE | STANDARD: | PRT: | 309 AA. | |
| AC P42082; | 01-NOV-1995 (Rel. 32, | Created) | | |
| DT DT | 01-NOV-1995 (Rel. 32, | Last sequence update) | | |
| Dt Dt | 01-OCT-2000 (Rel. 40, | Last annotation update) | | |
| DE T LYMPHOCTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2 | | | | |
| DE ANTIGEN) (EARLY T CELL COSTIMULATOR MOLECULE-1) (ETC-1). | | | | |
| CD86. | | | | |
| OS Mus musculus (Mouse). | | | | |
| CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| OX NCBI_TaxID=10090; | | | | |
| RN RN | [1] | | | |
| RP SEQUENCE FROM N.A. | | | | |
| RX MEDLINE=94065585; PubMed=7504059; | | | | |
| RA Freeman G.J., Borriello F., Hodess R.J., Reiser H., Gribsen J.G., | | | | |
| RA Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszlo G., Lombard L.A., | | | | |
| RA Wang S., Gray G.S., Nadler L.M., Sharpe A.H.; | | | | |
| RT "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates | | | | |
| TJ T cell proliferation and interleukin 2 production."; | | | | |
| RL J. Exp. Med. 178:2185-2192(1993). | | | | |
| RN RN | [2] | | | |
| RP SEQUENCE FROM N.A. | | | | |
| RC STRAIN=129; | | | | |
| RX MEDLINE=96094437;. PubMed=7499829; | | | | |
| RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.; | | | | |
| RT "Differential expression of alternate mb7-2 transcripts."; | | | | |
| RL J. Immunol. 155:5490-5497(1995). | | | | |
| RN RN | [3] | | | |
| RP SEQUENCE OF 7-309 FROM N.A. | | | | |
| RX MEDLINE=94230971; PubMed=7513726; | | | | |
| RA Chen C., Gaul A., Shen L., Nabavi N.; | | | | |
| RT "Molecular cloning and expression of early T cell costimulatory | | | | |
| J molecule-1 and its characterization as B7-2 molecule."; | | | | |
| RL J. Immunol. 152:4929-4936(1994). | | | | |
| - FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION. BY BINDING CD28 OR CTLA-4, MAY PLAY A CRITICAL ROLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION. | | | | |
| - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. | | | | |
| - TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS. | | | | |

[illegible]

| | | | | | |
|------|----------------------------------------------------------------------------------|---------------------------------------------------------------|-------------------------|--------------------------|----------------------|
| | FT | DWAIN | 660 | 727 | FIRONCTIN TYPE-III. |
| | FT | DISULFD | 441 | 96 | PROBABLE. |
| | FT | DISULFD | 139 | 189 | PROBABLE. |
| | FT | DISULFD | 235 | 287 | PROBABLE. |
| | FT | DISULFD | 329 | 385 | PROBABLE. |
| | FT | DISULFD | 426 | 479 | PROBABLE. |
| | FT | CARBOHD | 222 | 222 | N-LINKED (GLCNAC. .) |
| | FT | CARBORHT | 315 | 315 | (POTENTIAL). |
| | FT | CARBONBD | 347 | 347 | N-LINKED (GLCNAC. .) |
| | FT | CARBONDH | 423 | 423 | (POTENTIAL.) |
| | FT | CABOHND | 449 | 449 | N-LINKED (GLCNAC. .) |
| | FT | CABOHNHD | 478 | 478 | (POTENTIAL.) |
| | FT | CONFLICT | 215 | 215 | O -> R (IN REF. 2). |
| | FT | CONFLICT | 239 | 239 | G -> R (IN REF. 2). |
| | FT | CONFICT | 490 | 490 | L -> F (IN REF. 2). |
| | FT | . CONFLICT | 599 | 600 | OG -> R (IN REF. 3). |
| | FT | CONFLICT | 720 | 721 | MISING (IN REF. 3). |
| | FT | CONFLCIT | 811 | 811 | G-> A (IN REF. 3). |
| SQ | SEQUENCE | 848 AA; | 93360 MM; | 68D2FC0CE6C1CA2AD CRC64; | |
| | Query Match | Best Local Similarity | 8.6%; Score 135; | DB 1; | Length 848: |
| | Matches | 64; | Conservative | 23.2%; | Pred. No. 0.0027; |
| | | | 49; | Mismatches | 111; |
| | | | | Indels | 52; |
| | | | | Gaps | |
| OY | 63 | STVTTVASAGNIGEGILSCTF-----EPDIKLSDVIOWLKEGVLGVHEFKESKDE | 116 | | |
| | I : I : | I : I : I : I : I : I : I : I : I : I : I : I : I : I : | | | |
| Db | 77 | SSSTLTLYNA-NIDDAGIKYCVMGEDSEASEATVANKIFOKIMFNAPPOEERGEDA | 135 | | |
| OY | 117 | ISEODEM-----FRGRTNFAODY---IYGNSLRKNQJLDAGTCYKCIIITSK | 163 | | |
| Db | 136 | VIVCVSVSSLPTTIWKRRGDVILLKVDRIPRVISNNYLQIRGIKKTKDEGTIRC---- | E 190 | | |
| OY | 164 | G----KGANLEYKTGAFSPE-----VNVDYN-ASSETLCEAFRPFOPPYVAS | 210 | | |
| | I : I : | I : I : I : I : I : I : I : I : I : I : I : I : I : I : | | | |
| Db | 191 | CHLARGELNKRDIOVIYVNPPTIQARKNIYMALNALGGASTLVCD--EGRPETMSMTK | 249 | | |
| OY | 211 | OVGDSANESEVSNTSFELSBNEMTAKVVSYLVNYVINNTYSCLMIENDIAK--ATGDIKYT | 268 | | |
| | I : I : | I : I : I : I : I : I : I : I : I : I : I : I : I : I : | | | |
| Db | 250 | DOEQLEGEDEDKEYIFSDSSQLFIKYV----DKNEAEFYICIAMENKAGEODATHLKVF | 305 | | |
| OY | 269 | E-----SEIKRSHLDLNLKSASKVCSS---FFAISW 297 | | | |
| | I : I : | I : I : I : I : I : I : I : I : I : I : I : I : I : I : | | | |
| Db | 306 | AKPRTYYENOAMLEBQVTLTCEASGPDPISITW 341 | | | |
| | I : I : | I : I : I : I : I : I : I : I : I : I : I : I : I : I : | | | |
| | RESULT 15 | | | | |
| | NCAL_BOVIN | ' | | | |
| ID | NCAL_BOVIN | STANDARD; | PRT; | 853 | AA. |
| AC | p31836; | | | | |
| DT | 01-JUL-1993 | (Rel. 26, | Created) | | |
| DT | 01-JUL-1993 | (Rel. 26, | Last sequence update) | | |
| DT | 15-JUL-1999 | (Rel. 38, | Last annotation update) | | |
| DE | NEURAL CELL ADHESION MOLECULE, 140 KDA ISOFORM PRECURSOR (N-CAM 140) (NCAM-140). | | | | |
| GN | NCAM1 OR NCAM. | | | | |
| OS | Bos taurus (bovine). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| CC | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; | | | | |
| OX | Bovdae; Bovinae; Bos. | | | | |
| RX | NCBI_TaxID=9913; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. | | | | |
| RC | TISSUE=Brain cortex. | | | | |
| RX | MEDLINE=89376239; PubMed=2776887; | | | | |
| RA | Lipkin V.M., Khramtsov N.V., Andreeva S.G., Moshnyakov M.V., | | | | |
| RA | Petukhova G.V., Rakitina T.V., Peshchenko E.A., Ishchenko K.A., | | | | |
| RA | Miroshenko S.F., Chernova M.N., Dranshtyna S.M.; | | | | |
| RT | "Calmodulin-independent bovine brain adenylate cyclase. Amino acid | | | | |
| RL | sequence and nucleotide sequence of the corresponding cDNA."; | | | | |
| FPBS | J Biol Chem. 264(9):69-73(1989); | | | | |
| RM | [2] | | | | |
| RP | SEQUENCE OF 20-36. | | | | |

RX MEDLINE-86140120: PubMed-3512556;
 RA Rougon G., Marshak D.R.;
 RT "Structural and immunological characterization of the amino-terminal
 domain of mammalian neural cell adhesion molecules.";
 RL J. Biol. Chem. 261:3396-3401(1986).
 RN [3]
 RP IDENTIFICATION AS N-CAM.
 RX MEDLINE-92111748; PubMed-1765159;
 RA Premont R.T.;
 RT "A bovine brain cDNA purported to encode calmodulin-insensitive
 adenylyl cyclase has extensive identity with neural cell adhesion
 molecules (N-CAMs).";
 RL FEBS Lett. 295:230-231(1991).
 CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
 CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
 CC NEURITES, ETC.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
 CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A CALMODULIN-
 CC INDEPENDENT ADENYLYL CYCLASE.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X16451; CAA34470.1; -.
 DR PIR: A32976; IJBONC.
 DR HSSP: P40189; IBOU.
 DR InterPro: IPR001777; -.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; 1g; 5.
 KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
 KW Immunoglobulin domain; Alternative splicing; Signal;
 FT SIGNAL 1 19
 FT CHAIN 20 853
 FT
 FT DOMAIN 20 719
 FT TRANSMEM 720 737
 FT DOMAIN 738 853
 FT DOMAIN 132 103
 FT DOMAIN 132 103
 FT DOMAIN 132 103
 FT DOMAIN 228 293
 FT DOMAIN 321 401
 FT DOMAIN 428 495
 FT DOMAIN 527 604
 FT DOMAIN 633 700
 FT DOMAIN 152 156
 FT DOMAIN 161 165
 FT DISULFID 41 96
 FT DISULFID 139 189
 FT DISULFID 235 286
 FT DISULFID 328 394
 FT DISULFID 435 488
 FT CARBOHYD 222 222
 FT CARBOHYD 314 314
 FT CARBOHYD 346 346
 FT CARBOHYD 432 432
 FT CARBOHYD 458 458
 FT CARBOHYD 487 487
 FT SEQUENCE 853 AA; 93893 MW; E12FD49231A7A368 CRC64;
 Query Match 8.4%; Score 132.5; DB 1; Length 853;
 Best Local Similarity 23.4%; Pred. No. 0.0043;
 Matches 65; Conservative 46; Mismatches 110; Indels 57; Gaps 14;

QY 63 SITVTIVASAGNIGEDILISCTF-----EPDIKLSDIYIOWLKEGVLGLVHEFEKGEKDE 116
 Db 77 SSETLTIYNA-NIDDAGIYKCVYTAEDGTESEATVVKIFQKLMFNNAPTPOEFRGEDEA 135
 QY 117 LSEQDEM-----FNGRTAVFADQV---IVGNASIRLKNVQLTDAGTYKCYITTSK 163
 Db 136 VIVCDVYSSLPPTIWKHKRGVILKRDVRFIVLNNYLIQIRGIKKTDGTYRC-----E 190
 QY 164 G----KGNNANLEKKTGAFSMPE-----VANDVN-ASSETLRCAAPRPFQPTVYMAS 210
 Db 191 GRIARGEINFDIOYIVVPTVQAROSIVNATANGOSVTLVCNA-BGFPEPTVSWRK 249
 QY 211 QVDGAFSEVSNTSPELNSENVYMKVSVLYVTINTYSCMIENDIAKATGDI----- 265
 Db 250 DGEQIEN-EDEKYLEFSDSSSEITIRK---DKNDEAEYVCIAEKKAGQDASHTLKYF 304
 QY 266 ---KTESIKRRSHLQILNSKASLCVSS---FFAISW 297
 Db 305 AKPKIT--YVENQTAMELEQVTLTCEASGDPIPSITW 340

Search completed: July 23, 2001, 10:12:20
 Job time: 22 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2001, 10:11:58 ; Search time 22.6 Seconds
(without alignments)
1808.949 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574

Sequence: 1 HASHAHSGRQRLHASTQI.....SFFAISMALLPLSPYLMK 309

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

1: SP-archaea:*

2: SP-bacteria:*

3: SP-fungi:*

4: SP-human:*

5: SP-invertebrate:*

6: SP-mammal:*

7: SP-mhc:*

8: SP-organellar:*

9: SP-phage:*

10: SP-plant:*

11: SP-rodent:*

12: SP-unclassified:*

13: SP-vertebrate:*

14: SP-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 2 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 3 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 4 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 5 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 6 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 7 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 8 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 9 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 10 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 11 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 12 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 13 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 14 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 15 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 16 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 17 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 18 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |
| 19 | 1425 | 90.5 | 282 | 4 | Q9H6B2 |

| | | | | | | |
|----|-------|------|-----|----|--------|---------------------|
| 20 | 195.5 | 12.4 | 275 | 11 | Q9JK39 | Q9JK39 mus musculus |
| 21 | 193 | 12.3 | 527 | 4 | Q90475 | Q90475 homo sapien |
| 22 | 192 | 12.2 | 329 | 6 | Q9XSX6 | Q9XSX6 felis silve |
| 23 | 192 | 12.2 | 332 | 6 | Q9GWM2 | Q9GWM2 felis silve |
| 24 | 189 | 12.0 | 586 | 4 | Q9HCY2 | Q9HCY2 homo sapien |
| 25 | 188.5 | 12.0 | 290 | 4 | Q9NZ07 | Q9NZ07 homo sapien |
| 26 | 186 | 11.8 | 523 | 4 | P78408 | P78408 homo sapien |
| 27 | 183 | 11.6 | 529 | 4 | Q90480 | Q90480 homo sapien |
| 28 | 181 | 11.5 | 280 | 6 | Q9TFF1 | Q9TFF1 canis famill |
| 29 | 178 | 11.3 | 452 | 11 | Q70355 | Q70355 mus musculus |
| 30 | 176 | 11.2 | 313 | 11 | Q35531 | Q35531 rattus norv |
| 31 | 175.5 | 11.1 | 455 | 4 | Q9UIR0 | Q9UIR0 homo sapien |
| 32 | 172 | 10.9 | 329 | 6 | Q9TFF2 | Q9TFF2 canis famill |
| 33 | 171.5 | 10.9 | 272 | 11 | Q70356 | Q70356 mus musculus |
| 34 | 171.5 | 10.9 | 432 | 4 | Q9T2C7 | Q9T2C7 homo sapien |
| 35 | 169.5 | 10.8 | 284 | 6 | Q9GLJ3 | Q9GLJ3 bos taurus |
| 36 | 168.5 | 10.7 | 391 | 11 | Q35441 | Q35441 mus musculus |
| 37 | 166 | 10.5 | 326 | 11 | Q70358 | Q70358 mus musculus |
| 38 | 163 | 10.4 | 305 | 7 | Q98261 | Q98261 homo sapien |
| 39 | 160.5 | 10.2 | 325 | 6 | Q92838 | Q92838 sus scrofa |
| 40 | 153.5 | 9.8 | 325 | 11 | Q70359 | Q70359 mus musculus |
| 41 | 152.5 | 9.7 | 143 | 4 | Q9NU62 | Q9NU62 homo sapien |
| 42 | 151 | 9.6 | 339 | 13 | Q73892 | Q73892 gallus galli |
| 43 | 150.5 | 9.6 | 240 | 13 | Q73891 | Q73891 gallus galli |
| 44 | 149.5 | 9.5 | 396 | 6 | Q46405 | Q46405 bos taurus |
| 45 | 148 | 9.4 | 439 | 13 | Q57349 | Q57349 gallus galli |

ALIGNMENTS

| RESULT | 1 | PRELIMINARY: | PRT: | 282 AA. |
|--------|----------------------------------------------------------------------|--------------|------|---------|
| ID | Q9H6B2 | | | |
| AC | Q9H6B2 | | | |
| DT | 01-MAR-2001 (TREMBLrel. 16, Created) | | | |
| DT | 01-MAR-2001 (TREMBLrel. 16, Last sequence update) | | | |
| DE | CDNA: FLJ22418 FIS, ClONE HNC08590. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| OX | NCBI_Taxid=9606; | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Kawabata A., Hiki T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., | | | |
| RA | Okitani R., Ota T., Suzuki Y., Ohayashi M., Nishi T., Shibahara T., | | | |
| RA | Tanaka T., Nakamura Y., Isegai T., Sugano S.; | | | |
| RT | "NEO human cDNA sequencing project." | | | |
| RL | Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AK026071; BAB15349.1; " | | | |
| SO | SEQUENCE 282 AA; 30893 MW; 6F9066999A1E9DB4 CRC64; | | | |

| | | | | |
|-----------------------|--------------|-----------------------------------------------------------|---------------|-------------|
| Query Match | 90.5%; | Score 1425; | DB 4; | Length 282; |
| Best local Similarity | 99.6%; | Pred. No. 3.5e-110; | | |
| Matches 281; | Conservative | 0; | Mismatches 1; | Indels 0; |
| | | | Gaps 0; | |
| QY | 28 | MASLGIILFMSITSIITIIAGATALLTGISGRHSITVTYASAGNIGEDTLSTFEP | 87 | |
| DB | 1 | MASLGIILFMSITSIITIIAGATALLTGISGRHSITVTYASAGNIGEDTLSTFEP | 60 | |
| QY | 88 | DILSLIVLQWLEKGVGLVHEFEKEDLSDEDEFGRRTAVFADQVIVGNASLRLKNV | 147 | |
| DB | 61 | DILSLIVLQWLEKGVGLVHEFEKEDLSDEDEFGRRTAVFADQVIVGNASLRLKNV | 120 | |
| QY | 148 | QLTDACTYCYITTSKGNANLEYTGAFSMPDEVVDYNASSETLRCAPRFPOPTVY | 207 | |
| DB | 121 | QLTDACTYCYITTSKGNANLEYTGAFSMPDEVVDYNASSETLRCAPRFPOPTVY | 180 | |
| QY | 208 | MASOVQGANFSEVSTFSELSNENVTMKRVSVLYVNTINNTYSCMIENDIKATGDIVY | 267 | |
| DB | 181 | MASOVQGANFSEVSTFSELSNENVTMKRVSVLYVNTINNTYSCMIENDIKATGDIVY | 240 | |

OY 268 TESEIKRSHLOLNSKSLCVSSFFPAISWALLPLSPYIMLK 309
DB 241 TESEIKRSHLOLNSKSLCVSSFFPAISWALLPLSPYIMLK 282

RESULT 2
O9NM06 PRELIMINARY; PRT: 220 AA.
AC O9NM06:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CDNA FLJ20685 F15, CLONE KAIJA109.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ILEAL, MUCOSA;
RA Taniguchi A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
RA Hiraio M., Ohmori Y., Ota T., Suzuki Y., Ohayashi M., Nishi T.,
RA Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.,
RT "NEDO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK000692; BAA91323.1; -
DR InterPro; IPR003006; -
DR InterPro; IPR003006; -
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; Ig_1.
SQ SEQUENCE 220 AA; 24979 MW; 66967620E130B515 CRC64;

Query Match 14.3%; Score 225; DB 4; Length 220;
Best Local Similarity 31.1%; Pred. No. 5.7e-11;
Matches 61; Conservative 32; Mismatches 81; Indels 22; Gaps 7;

OY 73 GNIGEDGILSCFEPDIKSLDIVIOMLKEGVGLVHEFEKGEKDELSEODEMFRGTAVFA 132
DB 41 GLRDEDDILPSSFE--RGSEVYIMHKYQDSY-KVHSYKSGDHLSEODPRANRTSLFY 96
OY 133 DOVYGNASLRKKNQOLDAGTYKCIITTSKGGANLEKYGAFSMEPVNVYNASSET 192
DB 97 NEIQGNASLFEFRVSLDEGIYTCYGAIOVITNKVLAQVFLTPMKYKRNNTSF 156
OY 193 LRCEAPRPFPPPTVMAVSQVDGA---NFSEV-SNTSEFELSENVTMKVSVLYNVT-I 246
DB 157 LICSVLSVYPRPIITW--KMDNTPISENNMETGSLDPSINSP-----LNTIGS 204
OY 247 NNTYSCMIENDIAKAT 262
DB 205 NSSYECTIENSLKQT 220

RESULT 3
O9UM44 PRELIMINARY; PRT: 414 AA.
AC O9UM44:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HERV-H LTR ASSOCIATING PROTEIN 2.
GN HMLA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99375318; PubMed=10444326;
RA Mager D.L., Hunter D.G., Schertzer M., Freeman J.D.;
RT "Endogenous retroviruses provide the primary polyadenylation signal

RT for two new human genes (HMLA2 and HMLA3).".
RL Genomics 59:255-263(1999).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF126162; AAB48396.1; -
DR InterPro; IPR001039; -
DR InterPro; IPR003006; -
DR InterPro; IPR003006; -
DR Pfam; PF00047; Ig_2.
DR Prodom; PD000050; -1.
DR SMART; SM00410; IG_1like; 1.
SQ SEQUENCE 414 AA; 46850 MW; D645383E1562E70E CRC64;

Query Match 14.3%; Score 225; DB 4; Length 414;
Best Local Similarity 31.1%; Pred. No. 1.4e-10;
Matches 61; Conservative 32; Mismatches 81; Indels 22; Gaps 7;

OY 73 GNIGEDGILSCFEPDIKSLDIVIOMLKEGVGLVHEFEKGEKDELSEODEMFRGTAVFA 132
DB 41 GLRDEDDILPSSFE--RGSEVYIMHKYQDSY-KVHSYKSGDHLSEODPRANRTSLFY 96
OY 133 DOVYGNASLRKKNQOLDAGTYKCIITTSKGGANLEKYGAFSMEPVNVYNASSET 192
DB 97 NEIQGNASLFEFRVSLDEGIYTCYGAIOVITNKVLAQVFLTPMKYKRNNTSF 156
OY 193 LRCEAPRPFPPPTVMAVSQVDGA---NFSEV-SNTSEFELSENVTMKVSVLYNVT-I 246
DB 157 LICSVLSVYPRPIITW--KMDNTPISENNMETGSLDPSINSP-----LNTIGS 204
OY 247 NNTYSCMIENDIAKAT 262
DB 205 NSSYECTIENSLKQT 220

RESULT 4
O00481 PRELIMINARY; PRT: 513 AA.
AC O00481:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BURYRPHILIN.
GN BTF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruddy D.A., Kronmal G.S., Lee V.K., Muntler G.A., Quintana L.,
RA Domingo R., Meyer N.C., Basava A., McClelland E., Fullan A.,
RA Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchihashi Z.,
RA Wolff R.K., Schatzman R.C., Feder J.N.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; U90552; AAB53430.1; -
DR InterPro; IPR000107; -
DR InterPro; IPR001870; -
DR InterPro; IPR003006; -
DR Pfam; PF00047; Ig_1.
DR Pfam; PF00622; SPRY_1.
DR PRINTS; PR01407; BURYRPHILINCUF.
DR SMART; SM00449; SPRY_1.
SQ SEQUENCE 513 AA; 57762 MW; CD334D7727CD1F63 CRC64;

Query Match 14.2%; Score 223; DB 4; Length 513;
Best Local Similarity 26.4%; Pred. No. 2.7e-10;
Matches 69; Conservative 44; Mismatches 108; Indels 40; Gaps 10;

OY 62 HSIYTVTVASAGNI-----GEGDILSCFEPDIKSLDIVIOMLKEGVGLVHEFEKGEKDEL 117

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Db      HSAGSVLCPGSEPTILAMVGEDADLPCHLEFPFMSAFTMLKWNSSSLRQVYVNYAAGKEVE 86
       27 HSAGSVLCPGSEPTILAMVGEDADLPCHLEFPFMSAFTMLKWNSSSLRQVYVNYAAGKEVE
Oy      118 SEQDMEFGKRAVAFQDOYIVGNASLRKLNVLTDAGTKCYITTSKGNANLEKKGAF 177
       118 SEQDMEFGKRAVAFQDOYIVGNASLRKLNVLTDAGTKCYITTSKGNANLEKKGAF
Db      87 DROSAPYRGKRTSILDGDTAGCAALRIHNVTASDGGKYLCEYQDDDFEYKALVELKVAL 146
       87 DROSAPYRGKRTSILDGDTAGCAALRIHNVTASDGGKYLCEYQDDDFEYKALVELKVAL
Oy      178 SMEPEVNV---YNASSETLRCEAPRPPOPIYVMASSQDQGANFSESVNTPFLSENVT 234
       178 SMEPEVNV---YNASSETLRCEAPRPPOPIYVMASSQDQGANFSESVNTPFLSENVT
Db      147 G-SDLHVYKGTGGKCGIHLECKRSTGMYRPOPOQWSN--NKGEN---IPVPEAVVADG 200
       147 G-SDLHVYKGTGGKCGIHLECKRSTGMYRPOPOQWSN--NKGEN---IPVPEAVVADG
Oy      235 MKVV--SVLYNVTINNTFSCHIENDIAKATGDIKYTESEIKRSHLQILNSKASLVSS- 291
       235 MKVV--SVLYNVTINNTFSCHIENDIAKATGDIKYTESEIKRSHLQILNSKASLVSS-
Db      201 LYAVAAASYIMRRSSSEGVSCI-----RSSLLGLEKTAISIDIAP 240
       201 LYAVAAASYIMRRSSSEGVSCI-----RSSLLGLEKTAISIDIAP
Oy      292 FF--AISW--ALLPLSPYML 308
       292 FF--AISW--ALLPLSPYML
Db      241 FFERSAQRWIALAFLRLPYLL 261
       241 FFERSAQRWIALAFLRLPYLL
RESULT      5
O9HCY1      PRELIMINARY; PRT; 513 AA.
AC      O9HCY1.
ID      01-MAR-2001 (Tremblrel. 16, Created)
DT      01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT      01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE      DJA5P21.3 (BUTYROPHILIN, SUBFAMILY 3, MEMBER A1).
GN      BT3A1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      (1)
RP      SEQUENCE FROM N.A.
RA      Phillips S.;
RL      Submitted (JUN-2000) to the EMBL/GenBank/DBAJ databases.
DR      EMBL; AL021917; CAC03424.1; -.
SO      SEQUENCE 513 AA; 57677 MW; 80834D70526D1F6F CRC64;

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QY 82 SCTFFPDILSDIVIQWLKEVGLVHEKEGKDELSEODEMFRGTAVFADQVYGNAS 141
 DB 49 PCHLSPMSARSLDIRIMRHQVSEIYHRRNGEDLYGDMEEVYGTETLVGRGLSGRDL 108
 QY 142 LRLKNVQLDCTGYCYITTSKGNANLEYTGAF-SMPEVND-YNASSETLRCEAPR 199
 DB 109 LRISGRPSDDQGYCTVADGSSYGEATYDLEVSATGSPQLSLEYEGGIRVYCRSAG 168
 QY 200 WFPQPTVWASQVDOGANESEVSN-T-SFE---LNSENVTKVSVLYNVTINN---TYS 251
 DB 169 WYPREVLWKD---PGQHLPYSQRYSPFDERGLFTEDEVYI-----VTGDNROGKMS 218
 QY 252 CMLENDIAKATGDIKVTSEIKRRSHLOLNKASLVS-FP-----AIS 296
 DB 219 CVARN-----SHLN-QEOETSLHISAPFHNARPMWGVQVLLVLS 258
 QY 297 WALLPLSPYL 306
 DB 259 GVLGLGAVL 268

RESULT 8
 ID 046535 PRELIMINARY: PRT: 286 AA.
 AC 046535.
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE BUTYROPHILIN (FRAGMENT).
 GN BTN.
 OS Bos taurus (bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Husaini Y., Wilkins R.J., Davey H.W.;
 RL Submitted (DCC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AF037402; AAB92578.1; -.
 DR InterPro: IPR003006; -.
 DR InterPro: IPR003596; -.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Igv; 1.
 FT NON_TER 286
 FT SEQUENCE 286 AA: 32286 MW: 563DA4F372CA353D CRC64:

Query Match 13.9%; Score 219.5; DB 6; Length 286;
 Best Local Similarity 25.0%; Pred. No. 2.3e-10;
 Matches 49; Conservative 48; Mismatches 94; Indels 5; Gaps 4;
 QY 75 IGEGLISCTEPPDKLSDIYQWLKEVGLVHEFEKGEKDELSEODEMFRGTAVFADQ 134
 DB 42 VGEDELPCRLSPNSANGMELRMFRKRYSPAVFVSREGQEGEGEMAEYRGVSLVEDH 101
 QY 135 VIVGNASLRKLVQLTDAGTKCYITTSKGNANLEYTGAF-SMPEVNDYNNASS-E-T 192
 DB 102 IAEGVAVRIGQEVKASDGEGRCEFRQDENYEATVHLKVALGSDPHISMKVQESGEIQ 161
 QY 193 LRCEAPRMFPQPTVWASQVDOGANESEVSNSEFLENSENVTKVSVLYNVTINNFTSC 252
 DB 162 LECTSVGVYPERQVOW--RTNHRGEFPMSESRNDEEGTLFVRSVYLIIRDSMKNV-SC 218
 QY 253 MIENDIAKATGDIKVT 268
 DB 219 CIRNLLGOEKDVEVS 234

RESULT 9
 P78409

ID P78409 PRELIMINARY: PRT: 731 AA.
 AC P78409;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE BUTYROPHILIN.
 GN BT3.3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98044204; PubMed=9382921;
 RA Tazi-Ahmini R., Henry J., Offer C., Bouissou-Bouchouata C.,
 RA Mather I.H., Pontarotti P.;
 RT "Cloning, localization, and structure of new members of the
 RT butyrophilin gene family in the juxta-telomeric region of the major
 RT histocompatibility complex."
 CC Immunogenetics 47:55-63(1997).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: U97502; AAC02656.1; -.
 DR EMBL: U97500; AAC02656.1; JOINED.
 DR EMBL: U97501; AAC02656.1; JOINED.
 DR EMBL: U90143; AAC02651.1; -.
 DR InterPro: IPR000107; -.
 DR InterPro: IPR001870; -.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF00622; SPRY; 1.
 DR PRINTS: PR01407; BUTYRPHILNCDF.
 DR SMART: SM00449; SPRY; 1.
 SQ SEQUENCE 731 AA: 81393 MW: 2F0E0A32B73685F0 CRC64:

Query Match 13.7%; Score 215.5; DB 4; Length 731;
 Best Local Similarity 25.0%; Pred. No. 1.8e-09;
 Matches 62; Conservative 49; Mismatches 110; Indels 27; Gaps 9;
 QY 46 LAGATA-LIIGGIGSRHSITTYTASA-----GNIGEDGILSCTFFPDIKIS 92
 DB 1 MASSLAFLNLNPHVS-LFLVQLLTPCSAQFVLAGSPGPIAIVGDEADLPCHLFTMSAE 59
 QY 93 DIVIOLKRGVGLVHEFEKGEKDELSEODEMFRGTAVFADQVYGNASLRKLVQLD 152
 DB 60 TWELKRWSSLRQVAVYVADGKEVEYROSAPYRGRTSLRDGTTGKAKALRIHNTASDS 119
 QY 153 GYKCYIITTSKGNANLEYTGAFSMPEVND---YNASSETLRCEAPRMFPQPTVWVA 209
 DB 120 GKYLCTYFQHGDPYEKAPVLEKVALG-SDLHEVAGYDGGIHLBCRSRGWYRQPIKMS 178
 QY 210 SOVDGANESEVSNSEFLENSENVTKVY--SVLYNVTINNFTSCMIENDI--AKATGDI 265
 DB 179 D---SKGENIPAVEG---PVNVYGVGLVAVPPVIMTGTSGGVCITINSLIGLEKTASI 233
 QY 266 KYTESEIK 273
 DB 234 STADPFIO 241

RESULT 10
 ID 000478 PRELIMINARY: PRT: 584 AA.
 AC 000478.
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE BUTYROPHILIN.
 GN BT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBL_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ruddy D.A., Kronmal G.S., Lee V.K., Mintier G.A., Quintana L.,
 RA Domingo R., Meyer N.C., Basava A., McClelland E., Fullan A.,
 RA Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchinashi Z.,
 RA Wolff R.K., Schatzman R.C., Feder J.N.;
 RN Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RL (2)
 RP SEQUENCE FROM N.A.
 RA Phillips S.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: U90548; AAB53426.1; -
 DR EMBL: AL021917; CAI17273.1; -
 DR InterPro: IPR000107; -
 DR InterPro: IPR001870; -
 DR InterPro: IPR003006; -
 DR Pfam: PF00047; 1g; 1.
 DR Pfam: PF00622; SPRY; 1.
 DR PRINTS: PRO1407; BUTYPHLNCDF.
 DR SMART: SM00449; SPRY; 1.
 SQ SEQUENCE 584 AA; 65001 MW; 2B279B9141E0327F CRC64;

Query Match 13.6%; Score 213.5; DB 4; Length 584;
 Best Local Similarity 24.6%; Pred. No. 2e-09;
 Matches 60; Conservative 50; Mismatches 107; Indels 27; Gaps 9;

QY 46 LAQAIA-LIIGFISGRHSITVTVA-----GNGEGDILSCTEPDIKLS 92
 DB 3 MASSLAFLILNFHVS-LFLVQLTTPCSAOPSVLPGSPILAMWGEDADLPCHFPPTMSAE 61
 QY 93 DIYIOMLKEGVGLVHEFEKDELSEODEMFRGRTAVFAOYIVNASLRKNVQTFDA 152
 DB 62 TMLLRWVSSLRQVNVYADGKEVEDROSAPYGRGISILDGTTAGKAALRIHNVASDS 121
 QY 153 GTYKCIYITSKGKGNANLEYKTGAFSMEPVNV--YNASSETLRCEAPWFPQPIYVMA 209
 DB 122 GKLYCFQDDDFEKAALVELKVAALG-SDLHIEVKGEGDGIHLECSGTCWYPOQIKWS 180
 QY 210 SQYDOGANSEVNTSELSNSENTYMKV--SYLVNTINNTYSCMIENDI--AKATGDI 265
 DB 181 D--TKGENIPAV--EAPVADGVGLYAAVAAYIMRSGSGVSCITIRNSILGLEKTAI 235
 QY 266 KYTE 269
 DB 236 SIAD 239

RESULT 11
 ID 09H458 PRELIMINARY; PRT; 526 AA.
 AC 09H458;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE BK14H9.2 (BUTYROPHILIN, SUBFAMILY 1, MEMBER A1).
 GN BTN1A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBL_TaxID=9606;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Tracey A.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL121936; CAC16802.1; -
 SQ SEQUENCE 526 AA; 58960 MW; 4585D5CE88A2ECA4 CRC64;

Query Match 13.3%; Score 209.5; DB 4; Length 526;

Best Local Similarity 26.6%; Pred. No. 3.6e-09;
 Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;
 QY 75 IGEDGILSCTFEPPDIKLSLIVIOMLKEGVGLVHEFEKDELSEODEMFRGRTAVFADQ 134
 DB 42 VGEDADLPCHLPFTMSAEHLEKLVSSLSLQVNVYADGKEVEDROSAPYGRGISILRDG 103
 QY 135 VIVGNASLRKNVQIADAGTYKCIYITSKGKGNANLEYKTGAF-SMEPVNVYNASSE-T 192
 DB 102 IAKGRAVALRIRGVASDGEYTCFFREDGSYEALVHLKVAALGSPDHISMVOENGEIC 161
 QY 193 LREAPRWFPQPIYVNASQYDOGANSEVNTSELSNSENTYMKVSYLVNTINNTYSC 252
 DB 162 LECTSVGWPEPQVW--RTSKGKEFPSTSE-SRNPDEGLFTVAASVILIRTSANVSC 218
 QY 253 MIEN 256
 DB 219 YION 222

RESULT 12
 ID 09NR44 PRELIMINARY; PRT; 334 AA.
 AC 09NR44;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE BUTYROPHILIN, SUBFAMILY 3, MEMBER A2.
 GN BTN3A2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBL_TaxID=9606;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Rhodes D.A., Stammers M., Malcherek G., Beck S., Trowsdale J.;
 RT "Genomic structure of the btf (butyrophilin-like) gene cluster on
 human chromosome 6.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF257505; AAF76140.1; -
 DR InterPro: IPR003006; -
 DR InterPro: IPR003599; -
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00409; IG; 1.
 SQ SEQUENCE 334 AA; 36399 MW; 95CFE887DB0DBAE4 CRC64;

Query Match 13.2%; Score 208.5; DB 4; Length 334;
 Best Local Similarity 26.1%; Pred. No. 2.3e-09;
 Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

QY 75 IGEDGILSCTFEPPDIKLSLIVIOMLKEGVGLVHEFEKDELSEODEMFRGRTAVFADQ 134
 DB 44 VGEDADLPCHLPFTMSAEHLEKLVSSLSLQVNVYADGKEVEDROSAPYGRGISILRDG 103
 QY 135 VIVGNASLRKNVQIADAGTYKCIYITSKGKGNANLEYKTGAF-SMEPVNV-DYNASSET 192
 DB 104 ITGAKALRIHNVYASDSGYLYCFQDGFYEKALVELKVAALGSNLHVEVKGEGDGIH 163
 QY 193 LREAPRWFPQPIYVW-----ASQYDOGANSEVNTSELSNSENTYMKVSV 240
 DB 164 LECRSTGWYPOPIOWGNAGENIPAVEAVVADGVGLYEVA-----ASV 208
 QY 241 LVNVNTINNTYSCMIENDI--AKATGDIKYTE 269
 DB 209 IMKSGSGEVSCITIRNSILGLEKTAISID 239

RESULT 13
 ID 000477 PRELIMINARY; PRT; 319 AA.
 AC 000477;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMblrel. 04, last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
DE BUTYROPHILIN.
GN BTf4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
SQ
[1]
RP SEQUENCE FROM N.A.
RA Ruddy D.A., Kromal G.S., Lee V.K., Muttler G.A., Quintana L.,
Domínguez R., Meyer N.C., Basava A., McClelland E., Fullan A.,
Mape F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchinashi Z.,
Wolfe R.K., Schatzman R.C., Feder J.N.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL: U90546; AAB53424.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003599; -
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00409; 1g; 1.
SQ SEQUENCE 319 AA; 34734 MW; 1697EF524F558749 CRC64;

Query Match 13.2%; Score 207.5; DB 4; Length 319;
Best Local Similarity 26.1%; Pred. No. 2.7e-09;
Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

QY 75 IGEDGLSTFEPFDIKLSIDIVIQMLKEGVLGVHFEKSGKDELSDQEMFRGRTAVFAQD 134
DB 44 VEDDADLPCHLPPTMSAETMEKLVSSSLRQVYVYADKEVEDQSAFYRGRTSILRDG 103
QY 135 VIVGNASLRKLVNLTDACTGYCIITTSKGNANLEYRTGAF-SMPEYV-N-DYNASSET 192
DB 104 ITAGKAAALRIHNVATSDSKYLCYFQDGFYEKALVELKVALGSLNHLVEYVGEDGGIH 163
QY 193 LKCEAPRWFPPPTVWV-----ASQYDQGANSEVSNTSELSNENVTMKVSV 240
DB 164 LECRSTGWYPOQIOWSNKGENIPAVEAPVYADVGLGYEVA-----ASV 208
QY 241 LYNVTINNTYSCMIENDI--AKATGDIKYTE 269
DB 209 IMRGSSEGVSCITRNSLGLKETAISTAD 239
RESULT 14
ID 015338 PRELIMINARY; PRT; 357 AA.
AC 015338;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
DE BUTYROPHILIN.
GN BT3.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98044204; PubMed=9382921;
RA Tazi-Anhni R., Henry J., Offer C., Bouissou-Bouchouata C.,
Mather I.H., Pontarotti P.;
RT "Cloning, localization, and structure of new members of the
butyrophilin gene family in the juxta-telomeric region of the major
histocompatibility complex";
RL Immunogenetics 47:55-63(1997).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL: U97498; AAC02655.1; -
DR EMBL: U97499; AAC02655.1; JOINED.
DR InterPro: IPR003006; -.

DR InterPro: IPR003599; -
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00409; 1g; 1.
SQ SEQUENCE 357 AA; 39245 MW; A6BECA1D6B2C105 CRC64;

Query Match 13.2%; Score 207.5; DB 4; Length 357;
Best Local Similarity 26.1%; Pred. No. 3.1e-09;
Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

QY 75 IGEDGLSTFEPFDIKLSIDIVIQMLKEGVLGVHFEKSGKDELSDQEMFRGRTAVFAQD 134
DB 42 VEDDADLPCHLPPTMSAETMEKLVSSSLRQVYVYADKEVEDQSAFYRGRTSILRDG 101
QY 135 VIVGNASLRKLVNLTDACTGYCIITTSKGNANLEYRTGAF-SMPEYV-N-DYNASSET 192
DB 102 ITAGKAAALRIHNVATSDSKYLCYFQDGFYEKALVELKVALGSLNHLVEYVGEDGGIH 161
QY 193 LKCEAPRWFPPPTVWV-----ASQYDQGANSEVSNTSELSNENVTMKVSV 240
DB 162 LECRSTGWYPOQIOWSNKGENIPAVEAPVYADVGLGYEVA-----ASV 206
QY 241 LYNVTINNTYSCMIENDI--AKATGDIKYTE 269
DB 207 IMRGSSEGVSCITRNSLGLKETAISTAD 237

RESULT 15
ID P78410 PRELIMINARY; PRT; 359 AA.
AC P78410;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
DE BUTYROPHILIN PROTEIN.
GN BT3.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98044204; PubMed=9382921;
RA Tazi-Anhni R., Henry J., Offer C., Bouissou-Bouchouata C.,
Mather I.H., Pontarotti P.;
RT "Cloning, localization, and structure of new members of the
butyrophilin gene family in the juxta-telomeric region of the major
histocompatibility complex";
RL Immunogenetics 47:55-63(1997).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL: U90144; AAC02652.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003599; -
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00409; 1g; 1.
SQ SEQUENCE 359 AA; 39444 MW; 3CB2DA61322593B8 CRC64;

Query Match 13.2%; Score 207.5; DB 4; Length 359;
Best Local Similarity 26.1%; Pred. No. 3.1e-09;
Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

QY 75 IGEDGLSTFEPFDIKLSIDIVIQMLKEGVLGVHFEKSGKDELSDQEMFRGRTAVFAQD 134
DB 44 VEDDADLPCHLPPTMSAETMEKLVSSSLRQVYVYADKEVEDQSAFYRGRTSILRDG 103
QY 135 VIVGNASLRKLVNLTDACTGYCIITTSKGNANLEYRTGAF-SMPEYV-N-DYNASSET 192
DB 104 ITAGKAAALRIHNVATSDSKYLCYFQDGFYEKALVELKVALGSLNHLVEYVGEDGGIH 163
QY 193 LKCEAPRWFPPPTVWV-----ASQYDQGANSEVSNTSELSNENVTMKVSV 240
DB 162 LECRSTGWYPOQIOWSNKGENIPAVEAPVYADVGLGYEVA-----ASV 206
QY 241 LYNVTINNTYSCMIENDI--AKATGDIKYTE 269
DB 207 IMRGSSEGVSCITRNSLGLKETAISTAD 237

Mon Jul 23 13:51:15 2001

us-09-636-801-392.rspt

Page 7

Db 164 LECRSTGWTPOPOIONNAKENIPAVEAPVADGVGLYEVA-----ASV 208

OY 241 LYNVTINNTYSCMIENDI--AKATGDIKYTE 269

Db 209 IMRGSGEVSCIIIRNSLGLKXTASISAD 239

Search completed: July 23, 2001, 10:13:30
Job time: 92 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 23, 2001, 10:11:58 ; Search time 20.63 Seconds

(without alignments)
908.037 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574

Sequence: 1 HASAHASRQROHLSASTQT.....SSFAISWALLPLSPYLMK 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /SIDSR/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|---------|--------------------|
| 1 | 1574 | 100.0 | 309 | 21 | AA12556 | Human ovarian carc |
| 2 | 1431 | 90.9 | 282 | 21 | AA12557 | Human ovarian carc |
| 3 | 1431 | 90.9 | 282 | 21 | AA12557 | Human ovarian carc |
| 4 | 1431 | 90.9 | 282 | 21 | AA12557 | Human ovarian carc |
| 5 | 1431 | 90.9 | 282 | 21 | AA12557 | Human ovarian carc |
| 6 | 842.5 | 53.5 | 195 | 22 | AA65242 | Human PRO1291 (UNQ |
| 7 | 246 | 15.6 | 387 | 22 | AA67776 | Gene 47 related pe |
| 8 | 246 | 15.6 | 387 | 22 | AA67776 | Human gene 2 encod |
| 9 | 246 | 15.6 | 387 | 22 | AA67776 | Human membrane or |
| 10 | 241 | 15.3 | 316 | 20 | AA41705 | Human amyloid prec |
| 11 | 241 | 15.3 | 316 | 21 | AA44261 | Human PRO352 (UNQ3 |

| | | | | | | |
|----|-------|------|-----|----|----------|--------------------|
| 12 | 239 | 15.2 | 316 | 22 | AA67394 | Human gene 2 encod |
| 13 | 239 | 15.2 | 316 | 22 | AA67394 | Human amyloid prec |
| 14 | 232.5 | 14.8 | 534 | 22 | AA67417 | Human gene 2 encod |
| 15 | 225.5 | 14.3 | 466 | 21 | AA199413 | Human PRO1472 (UNQ |
| 16 | 225.5 | 14.3 | 466 | 22 | AA67577 | Human PRO1472. Ho |
| 17 | 225.5 | 14.3 | 466 | 22 | AA66162 | Protein of the Inv |
| 18 | 225 | 14.3 | 327 | 22 | AA680415 | Gene #1 associated |
| 19 | 225 | 14.3 | 349 | 22 | AA680414 | Gene #1 associated |
| 20 | 225 | 14.3 | 414 | 22 | AA680371 | Secreted protein e |
| 21 | 224.5 | 14.3 | 461 | 21 | AA65591 | Protein encoded by |
| 22 | 223 | 14.2 | 513 | 19 | AA678918 | Bovine butyrophill |
| 23 | 222.5 | 14.1 | 461 | 21 | AA65615 | Human secreted pro |
| 24 | 222.5 | 14.1 | 500 | 21 | AA69385 | Human PRO1347 (UNQ |
| 25 | 222.5 | 14.1 | 500 | 22 | AA67567 | Human PRO1347. Ho |
| 26 | 222.5 | 14.1 | 500 | 22 | AA66134 | Gene 47 related pe |
| 27 | 219.5 | 13.9 | 526 | 20 | AA67775 | Bovine butyrophill |
| 28 | 219.5 | 13.9 | 519 | 21 | AA697812 | Bovine butyrophill |
| 29 | 218 | 13.9 | 319 | 21 | AA65584 | BHR II protein en |
| 30 | 213.5 | 13.6 | 584 | 19 | AA678916 | Bovine butyrophill |
| 31 | 211.5 | 13.4 | 526 | 20 | AA67814 | Human butyrophill |
| 32 | 209 | 13.3 | 223 | 19 | AA671593 | Human myelin oligo |
| 33 | 207.5 | 13.2 | 319 | 19 | AA678917 | Bovine butyrophill |
| 34 | 207.5 | 13.2 | 331 | 19 | AA671592 | Human myelin oligo |
| 35 | 207.5 | 13.2 | 334 | 20 | AA69661 | Human secreted pro |
| 36 | 202 | 12.8 | 524 | 20 | AA697815 | Guinea pig butyrop |
| 37 | 199.5 | 12.7 | 250 | 22 | AA672646 | Murine B7-4 protei |
| 38 | 193 | 12.3 | 527 | 19 | AA678914 | Bovine butyrophill |
| 39 | 192 | 12.2 | 329 | 21 | AA632285 | Feline CD86 (B7-2) |
| 40 | 192 | 12.2 | 332 | 20 | AA632278 | Feline CD86 (B7-2) |
| 41 | 192 | 12.2 | 332 | 20 | AA641079 | Feline B7-2 protei |
| 42 | 188.5 | 12.0 | 290 | 22 | AA672645 | Human B7-4 membran |
| 43 | 183 | 11.6 | 523 | 19 | AA678915 | Bovine butyrophill |
| 44 | 182 | 11.6 | 245 | 22 | AA672644 | Human B7-4 secre |
| 45 | 181 | 11.5 | 280 | 20 | AA641078 | Canine B7-25 prote |

ALIGNMENTS

| | |
|---------|---------------------------------------------------------------------------------------------------------------------------------------------|
| RESULT | 1 |
| AA12556 | AA12556 standard; Protein; 309 AA. |
| ID | AA12556; |
| AC | AA12556; |
| DT | 07-NOV-2000 (first entry) |
| XX | |
| DE | Human ovarian carcinoma antigen OBE protein SEQ ID NO:392. |
| XX | |
| KW | Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis; |
| KW | tumour antigen; identification; cytosolic; gene therapy; vaccine. |
| XX | |
| OS | Homo sapiens. |
| PN | WO200036107-A2. |
| XX | |
| PD | 22-JUN-2000. |
| XX | |
| PF | 17-DEC-1999; 99WO-0530270. |
| XX | |
| PR | 17-DEC-1998; 98US-0215681. |
| PR | 17-DEC-1998; 98US-0216003. |
| PR | 23-JUN-1999; 99US-0338933. |
| PR | 24-SEP-1999; 99US-0404879. |
| XX | |
| PA | (CORI-) CORIXA CORP. |
| XX | |
| PI | Mitcham JL, King GE, Algate PA, Frudakis TN; |
| DR | WPI; 2000-431589/37. |
| XX | |
| PT | Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of |

PT cancer, preferably ovarian cancer -

XX
XX
PS Example 2; Page 205-206; 299pp; English.

CC The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytosolic activity and can be used in gene therapy and vaccines.
CC Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines
CC are useful for the prevention, diagnosis and treatment of cancer,
CC preferably ovarian cancer. AA69691 to AA70077 and AAB12552 to AAB12557
CC represent human ovarian carcinoma polynucleotides and proteins used in
CC the exemplification of the present invention.

XX
XX
SQ Sequence 309 AA:

Query Match 100.0%; Score 1574; DB 21; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.9e-131;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRORLHSASTOIRWEPSPAMASLGQILFWSIITSIITLACALILIGFGISG 60
DB 1 hasahasgrqrlhsastqirwepspamaslqllfwsllstlllagaalilifglsq 60

QY 61 RHSTIVTVASAGNIGEDGILSCFEPDIKLSDIYIQWLKEGVGLVHEFKEGKDELSEQ 120
DB 61 rhstltvtvasagnlgedgllscfepdklsdlylqwlkegvglvhefkegkdelseq 120

QY 121 DEMFGRTAVFADQYIVGNASRLKNNQLTDAQTYKCYITTSKGGNNLEKTKGAFSMP 180
DB 121 demfgrtafvadqyivgnasrlknvqltdaqtykcylltskkggnallekkgafsm 180

QY 181 EVNVVDYNASSETLRCEAPRMPQPTVYVNASQYDQGANFSEVSNFSFELNSEVNTMKVVS 240
DB 181 evnvvdynassetlrceaprfpqptvvasqydgnganfsevnfsfelnsevnmtkvsv 240

QY 241 LYNNVTINNTYSCMIENDIAKATGDIKVTSEIKRSHLQQLNSKASLCVSSFFAISWALL 300
DB 241 lynnvtinntyscmiendiakatgdiikvtseikrshlqqlnskaslcvsffaiswall 300

QY 301 PLSPYLMLK 309
DB 301 plspylmlk 309

RESULT 2
AAB12557
ID AAB12557 standard; Protein: 282 AA.

XX
XX
AC AAB12557;

XX
XX
DT 07-NOV-2000 (first entry)

XX
XX
DE Human ovarian carcinoma antigen O8E protein SEQ ID NO:393.

XX
XX
KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KW tumour antigen; identification; cytostatic; gene therapy; vaccine.

XX
XX
OS Homo sapiens.

XX
XX
PN WO200036107-A2.

XX
XX
PD 22-JUN-2000.

XX
XX
PF 17-DEC-1999; 99WO-US30270.

XX
XX
PR 17-DEC-1998; 98US-0215681.
PR 17-DEC-1998; 98US-0216003.
PR 23-JUN-1999; 99US-0338933.
PR 24-SEP-1999; 99US-0404879.

XX
XX
PA (CORI-) CORIXA CORP.

XX
PI Mitcham JL, King GE, Algate PA, Frudakis TN;
XX WPI; 2000-431589/37.

DR
XX
XX

PT Immunogenic portion of an ovarian carcinoma protein and the nucleic
CC acid encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer -

XX
XX
PS Example 2; Page 207; 299pp; English.

CC The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytosolic activity and can be used in gene therapy and vaccines.
CC Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines
CC are useful for the prevention, diagnosis and treatment of cancer,
CC preferably ovarian cancer. AA69691 to AA70077 and AAB12552 to AAB12557
CC represent human ovarian carcinoma polynucleotides and proteins used in
CC the exemplification of the present invention.

XX
XX
SQ Sequence 282 AA:

Query Match 90.9%; Score 1431; DB 21; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.3e-119;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWSIITSIITLACALILIGFISGRHSITVTVASAGNIGEDGILSCFEP 87
DB 1 maslqllfwsllstlllagaalilifglsgrhsitvtvasagnlgedgllscfep 60

QY 88 DIKLSDIYIQWLKEGVGLVHEFKEGKDELSEODEMFRGRTAVFADQYIVGNASRLKNN 147
DB 61 dklldlylqwlkegvglvhefkegkdelseqdemfgrtafvadqyivgnasrlknv 120

QY 148 QLTDAQTYKCYITTSKGGNNLEKTKGAFSMP EVNVVDYNASSETLRCEAPRMPQPTV 207
DB 121 qldaqtykcylltskkggnallekkgafsm evnvvdynassetlrceaprfpqptv 180

QY 208 WASOYDQGANFSEVSNFSFELNSEVNTMKVVS LYNNVTINNTYSCMIENDIAKATGDIK 267
DB 181 wasydgnganfsevnfsfelnsevnmtkvsv lynnvtinntyscmiendiakatgdi 240

QY 268 TSEIKRSHLQQLNSKASLCVSSFFAISWALLPLSPYLMLK 309
DB 241 tseikrshlqqlnskaslcvsffaiswallplspylmlk 282

RESULT 3
AAY66719
ID AAY66719 standard; Protein: 282 AA.

XX
XX
AC AAY66719;

XX
XX
DT 05-APR-2000 (first entry)

XX
XX
DE Membrane-bound protein PRO1291.

XX
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX
XX
OS Homo sapiens.

XX
XX
PN WO9963088-A2.

XX
XX
PD 09-DEC-1999.

XX
XX
PF 02-JUN-1999; 99WO-US12252.

XX
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087739.

PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
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PR 10-JUN-1998; 98US-0088824.
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PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
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PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
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PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089603.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
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PR 24-JUN-1998; 98US-0090538.
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PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
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PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.

PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
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PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091638.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0092182.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095285.
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PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
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PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
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PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098325.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.

XX PA (GETH) GENENTECH INC.
XX PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX PI Wood WI, Yuan J;
XX XX
DR WPI, 2000-072883/06.
DR N-PSDB; AAZ65059.
XX XX
PT Membrane-bound proteins and related nucleotide sequences -
XX PS claim 12, Fig 208; 822pp; English.
XX XX

CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIR
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO molecule inhibitors
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.

SO Sequence 282 AA:

Query Match 90.9%; Score 1431; DB 21; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.5e-119;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWMSIIITIIILAGAILIGFISGRHSITVTYVASAGNIGEDGILSCTFEP 87
DB 1 maslqgilfwslisllilagaalilgfgisgrhsilvtvasagnigedgilsctfep 60
QY 88 DIKLSDIVIOWLKEVGLVHFEKSGKDELSEODEMFRGRTAVFADQVIVGNASRLKRV 147
DB 61 dklldivlwkeglvghfkegkdelseodemfrtrtavfadvqivgnasrlrkvv 120
QY 148 QLTDACTYCYIITTSKGCNANLEKYGAFSMEPVNVVDYNASSETLRCAAPRWFPQPTVY 207
DB 121 qltdagtykcyiitstskgknanleyktgafsmpevnyvdynassetlrceaprwfpqptvv 180
QY 208 WASOVDOGANFSEVSWTSELSSENVTMKVSVLYNVNTINNTYSCMIENDIKAKAGDIKY 267
DB 181 wasqvdoganfevswtselnsenvtkmvsvlynvntinnyscmldndiakagtdikv 240
QY 268 TSEIKRRSHLOLNSKASLCVSSFFPAISWALLPLSPYIMLK 309
DB 241 tseikrrshlqlnksalcvssffaiswallplspylimlk 282

RESULT 4
AAB87555
ID AAB87555 standard; Protein; 282 AA.
XX
AC AAB87555;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1291.
XX
KW Human; PRO protein; mapping.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23328.
XX
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 07-DEC-1999; 99US-0169495.
PR 09-DEC-1999; 99US-0170262.
PR 11-JAN-2000; 2000US-0175481.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 03-MAR-2000; 2000US-0187202.

PR 25-APR-2000; 2000US-0199397.
PR 22-MAY-2000; 2000WO-US14042.
PR 05-JUN-2000; 2000US-0209832.

PA (GERTH) GENENTECH INC.

PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

DR WPI: 2001-183260/18.
DR N-PSDB: AAF92087.

PT Eighty four nucleic acids encoding PRO polypeptides, useful in
PT molecular biology, including use as hybridization probes, and in
PT chromosome and gene mapping.

PS Claim 12; Fig 60; 278bp; English.

CC The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping.

SO Sequence 282 AA:

Query Match 90.9%; Score 1431; DB 22; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.5e-119;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWMSIIITIIILAGAILIGFISGRHSITVTYVASAGNIGEDGILSCTFEP 87
DB 1 maslqgilfwslisllilagaalilgfgisgrhsilvtvasagnigedgilsctfep 60
QY 88 DIKLSDIVIOWLKEVGLVHFEKSGKDELSEODEMFRGRTAVFADQVIVGNASRLKRV 147
DB 61 dklldivlwkeglvghfkegkdelseodemfrtrtavfadvqivgnasrlrkvv 120
QY 148 QLTDACTYCYIITTSKGCNANLEKYGAFSMEPVNVVDYNASSETLRCAAPRWFPQPTVY 207
DB 121 qltdagtykcyiitstskgknanleyktgafsmpevnyvdynassetlrceaprwfpqptvv 180
QY 208 WASOVDOGANFSEVSWTSELSSENVTMKVSVLYNVNTINNTYSCMIENDIKAKAGDIKY 267
DB 181 wasqvdoganfevswtselnsenvtkmvsvlynvntinnyscmldndiakagtdikv 240
QY 268 TSEIKRRSHLOLNSKASLCVSSFFPAISWALLPLSPYIMLK 309
DB 241 tseikrrshlqlnksalcvssffaiswallplspylimlk 282

RESULT 5
AAB65242
ID AAB65242 standard; Protein; 282 AA.
XX
AC AAB65242;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1291 (UNQ659) protein sequence SEQ ID NO:291.
XX
KW Human; secreted and transmembrane protein; PRO: cytosolic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX

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PD 07-DEC-2000.
XX
XX 30-MAR-2000: 2000MO-US08439.
PR 02-JUN-1999: 99MO-US12252.
PR 23-JUN-1999: 99US-0141037.
PR 07-JUL-1999: 99US-0143048.
PR 20-JUL-1999: 99US-0144758.
PR 26-JUL-1999: 99US-0145698.
PR 28-JUL-1999: 99US-0146222.
PR 17-AUG-1999: 99US-0149396.
PR 15-SEP-1999: 99MO-US21090.
PR 15-SEP-1999: 99MO-US21547.
PR 08-OCT-1999: 99US-0158663.
PR 30-NOV-1999: 99MO-US28313.
PR 01-DEC-1999: 99MO-US28301.
PR 16-DEC-1999: 99MO-US30095.
PR 20-DEC-1999: 99MO-US30911.
PR 05-JAN-2000: 2000MO-US00219.
PR 06-JAN-2000: 2000MO-US00376.
PR 11-FEB-2000: 2000MO-US03565.
PR 18-FEB-2000: 2000MO-US04341.
PR 22-FEB-2000: 2000MO-US04414.
PR 24-FEB-2000: 2000MO-US04914.
PR 24-FEB-2000: 2000MO-US05004.
PR 02-MAR-2000: 2000MO-US05841.
PR 15-MAR-2000: 2000MO-US06884.
PR 20-MAR-2000: 2000MO-US07377.
PA (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnuyers L, Eaton DL,
PI Ferrara N, Fong S, Geider H, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Gurey AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart JA, Tumas D, Watanabe CK, Williams PM, Wood WI,
PI Zhang Z;
XX
XX MPI: 2001-032160/04.
DR N-PSDB; AAF44205.
XX
XX PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
XX Claim 12; Fig 208; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
XX Sequence 282 AA:
SQ
Query Match 90.9%; Score 1431; DB 22; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.5e-119;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
DB 61 dklstdivlqkvgvlgvlvhefkegkdelseqdemtrgrtavlfaqvlygnaslrlnkv 120
OY 148 QLTDACTKYCYIIITSKGGANLEKRTGAFSMEPVNDVYNAASSETLRCAPRPFPTVY 207
DB 121 qltdaglykcylltskxgkgnanleykrtgafsmpevndvynasasetlrceaprfpqltv 180
OY 208 WASOVGAGNFSEVSNFSFLENSENYTMKVSVLYXNTTNSCMTENDIAKATGDIKV 267
DB 181 wasqvqganfsevsntsfelnsenvtmkvsvlynvltlnlyscmlendiaakatgdiqv 240
OY 268 TSESEIKRSHLOLLNSKASCLVSSFALISWALLPLSPYLMLK 309
DB 241 tseelikrshlqlnksalcvsafaiswallplspylmlk 282
RESULT 6
AAB60776
ID AAB60776 standard; peptide; 195 AA.
XX
XX AAB60776;
AC 27-MAR-2001 (first entry)
XX
XX Gene 47 related peptide #2.
XX
XX Secreted protein; gene therapy; vaccine; cancer; leukemia;
KW autoimmune disease; allergy; inflammation; graft rejection;
KW hyperproliferation; cardiovascular; infection.
XX
XX Homo sapiens.
OS
XX
XX WO200076531-A1.
PN
XX 21-DEC-2000.
PD
XX
XX 01-JUN-2000: 2000MO-US15137.
PF
XX
XX 11-JUN-1999: 99US-0138625.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
PI
XX
XX MPI: 2001-071148/08.
DR
XX
XX Nucleic acids encoding 47 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
PT disease and diabetic retinopathy -
XX
XX Disclosure; Page 524-525; 525pp; English.
XX
XX The present invention relates to 26 secreted human proteins. The
CC proteins may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate polypeptide expression.
CC For example, they may be used in gene therapy or in vaccines.
CC Typical of diseases which are potentially treatable are cancers
CC (including leukemia), autoimmune diseases, allergies, inflammation,
CC graft rejection, hyperproliferation, cardiovascular diseases
CC (particularly critical limb ischemia and coronary disease) and any
CC involving abnormal angiogenesis, neurodegeneration and/or
CC infectious diseases.
XX
XX Sequence 195 AA:
SQ
Query Match 53.5%; Score 842.5; DB 22; Length 195;
Best Local Similarity 82.1%; Pred. No. 5.8e-67;
Matches 170; Conservative 3; Mismatches 9; Indels 25; Gaps 2;
```


PI Oka T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX WPI: 2001-093989/11.
DR N-PSDB: AAF93886.
XX
PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
XX gene therapy or as candidate target molecules in drug development -
PS Claim 1; SEQ ID 286; 609pp + CD ROM; English.
XX
CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by
CC AAF88317 - AAF88419. Included in the invention are primers
CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
CC cDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC protein/membrane protein expression. The nucleic acids and complementary
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC as antigens in the production of antibodies against them and in assays to
CC identify modulators (agonists and antagonists) of expression and
CC activity. The antibodies and antagonists may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay
CC (ELISA)). Examples of diseases which may be treated include rheumatoid
CC arthritis and diabetes.
XX
SQ Sequence 534 AA;

Query Match 15.68; Score 246; DB 22; Length 534;
Best Local Similarity 26.28; Pred. No. 1.5e-13;
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

YY 19 QIRPEPSPAMASLGQI-----LF--WSIIISIIILAGATALLIGFI---SGRHS 63
DB 175 evfqdgqgvpplgtvntsgmaneglfidvnsilrvlvgangtysclvrnpvlqgdahs 234
YY 64 ITVTTVAS-----AGNIGEDGILSCTF--EPDIRKSDIVIQMLKRGVLGLV 107
DB 235 vltlprqspigavevqvpdpvvalvgtdatlrcsfspgpfslaqnlilwqltdtkqlv 294
YY 108 HEFKEGDELSEODEMFRGRTAVPADOVIVGNASLRKNVQLTDAGTYKCYIIRSKGKN 167
DB 295 hsftegrd-----qgsayantalfpdlilagnaslrlqrvvadegsfctf-vslrdfigs 349
YY 168 ANLEYKTGA-FSMPEVNVN-----ASSETLRCEADRMFPQPTVWASQVDOGANSEV 221
DB 350 aavslqyaapyskpsmcllepklrlpgdltvltcsyrygpeaevfw--qdgqgvplltgn 407
YY 222 SNTSEFLENSEVIMKVVSVLYNVT-INNTYSCEMIENDIAK--ATGDIKVT 268
DB 408 vltcs-qmaneglfidvnsilrvlvgangtysclvrnpvlqgdahsvltl 456

RESULT 9
ID AAB27250 standard; Protein; 534 AA.
XX AAB27250;
AC
XX 27-MAR-2001 (first entry)
DT Human amyloid precursor protein protease SEQ ID NO: 4.
XX

KW Human; amyloid precursor protein protease; Alzheimer's disease;
KM neurodegenerative disease.

OS Homo sapiens.

PN W0200068266-A1.

PD 16-NOV-2000.

PF 09-MAY-2000; 2000WO-US06707.

PR 11-MAY-1999; 99US-0133423.

PA (ELIL) LILLY & CO ELI.

PI Becker GW, Hale JE, Heath WF, Johnstone EM, Little SP, Tu Y,
PI Yeh W, Yin T;

DR WPI: 2001-016080/02.
DR N-PSDB: AAC66922.

PT New amyloid precursor protein proteases and nucleic acids useful for
PT identifying amyloid precursor protein protease inhibitors for treating
PT or preventing Alzheimer's disease and other neurodegenerative diseases
XX
PS Claim 1; Page 7-9; 82pp; English.

XX
CC The present sequence is a human amyloid precursor protease protein.
CC Amyloid precursor protein builds up in the brain of individuals with
CC Alzheimer's disease, and the sequences of the invention can be used to
CC identify compounds which can be used to prevent and treat the disease. In
CC addition, they are suitable for use in the treatment of other
CC neurodegenerative diseases, Down's syndrome and hereditary cerebral
CC haemorrhage with amyloidosis of the Dutch-type (HCHWA-D).
XX
SQ Sequence 534 AA;

Query Match 15.68; Score 246; DB 22; Length 534;
Best Local Similarity 26.28; Pred. No. 1.5e-13;
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

YY 19 QIRPEPSPAMASLGQI-----LF--WSIIISIIILAGATALLIGFI---SGRHS 63
DB 175 evfqdgqgvpplgtvntsgmaneglfidvnsilrvlvgangtysclvrnpvlqgdahs 234
YY 64 ITVTTVAS-----AGNIGEDGILSCTF--EPDIRKSDIVIQMLKRGVLGLV 107
DB 235 vltlprqspigavevqvpdpvvalvgtdatlrcsfspgpfslaqnlilwqltdtkqlv 294
YY 108 HEFKEGDELSEODEMFRGRTAVPADOVIVGNASLRKNVQLTDAGTYKCYIIRSKGKN 167
DB 295 hsftegrd-----qgsayantalfpdlilagnaslrlqrvvadegsfctf-vslrdfigs 349
YY 168 ANLEYKTGA-FSMPEVNVN-----ASSETLRCEADRMFPQPTVWASQVDOGANSEV 221
DB 350 aavslqyaapyskpsmcllepklrlpgdltvltcsyrygpeaevfw--qdgqgvplltgn 407
YY 222 SNTSEFLENSEVIMKVVSVLYNVT-INNTYSCEMIENDIAK--ATGDIKVT 268
DB 408 vltcs-qmaneglfidvnsilrvlvgangtysclvrnpvlqgdahsvltl 456

RESULT 10
ID AAY41705 standard; Protein; 316 AA.
XX AAY41705;
AC
XX 07-DEC-1999 (first entry)
DT Human PRO352 protein sequence.
XX

DR N-PSDB: AAF91910.

XX Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers -
XX

PS Claim 11; Page 563-564; 607pp; English.

XX AAF91910 represent cDNAs corresponding to 52 human secreted
CC protein genes, and AAB87413 represent the proteins they encode.
CC AAB87414-AAB87454 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Pathological conditions can be diagnosed by determining the
CC amount of the new protein in a sample or by determining the presence of
CC mutations in the new genes. Specific uses are described for each of the
CC 52 genes, based on the tissues in which they are most highly expressed,
CC and include developing products for the diagnosis or treatment of
CC proliferative disorders, cancer, tumours, foetal and developmental
CC abnormalities, haematopoietic disorders, diseases of the immune system,
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC allergies, neurological disorders (e.g., Alzheimer's disease,
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC cardiovascular disorders, angiogenic disorders, kidney disorders,
CC gastrointestinal disorders, pregnancy-related disorders, endocrine
CC disorders, and infections. The proteins can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues, to identify their
CC cognate ligands or binding partners, and in chemotaxis, and can be used
CC as a food additive or preservative to modify storage properties.
CC Antibodies specific for a protein of the invention can be used in
CC alleviating symptoms associated with the disorders mentioned above, and
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC immunosorbent assay (ELISA). The present sequence represents a human
CC secreted protein of the invention.
XX

SQ Sequence 316 AA;

Query Match 15.2%; Score 239; DB 22; Length 316;

Best Local Similarity 27.5%; Pred. No. 3.1e-13;

Matches 71; Conservative 46; Mismatches 109; Indels 32; Gaps 9;

QY 20 IRMEPSPAMASLGQILFMSIISIIILAGATALLIGFGSGRHSITVTVASAGNIGEDG 79
Db 2 IIRGSPGPMG-----VHVGAAIGALWfcltgalevgvpedpvalvgtda 46
QY 80 ILSCYF--EPDIKLSDIYIQLKKEGVLGVHEFEKGEKDELSEQDEMFGRRTAVFADQYIV 137
Db 47 tlccsfspgfsfslaglnlwgldtkqlvhsfaegqd---qgsaayanrtalfpdliaq 102
QY 138 GNASRLKNNVQLTDAGTYKCYITTSKKGANLEKTKGA-FSMPEVNDYN-----ASSE 191
Db 103 gnasrlrlgrvrvadegsfctf-vslrldfgsaavslqvaaypskpsmtlepnkdlrpgdtv 161
QY 192 TLRCFAPRMFPQPTVYVMAQVDOGANFSEVSTSELSSENVTMKNVSVLVNVT-INNTY 250
Db 162 tlccssygygypaeavfw--qdgqgvyplcgnvts-qmanegldfvhslilrvlgangly 218
QY 251 SCMIENDIAKATGDIKVT 268
Db 219 sclvrnpvlgqdahesvt 236

RESULT 13

AAB27249

ID AAB27249 standard; Protein: 534 AA.

XX AAB27249;

XX 27-MAR-2001 (first entry)

XX Human amyloid precursor protein protease SEQ ID NO: 2.
DE
XX Human: amyloid precursor protein protease; Alzheimer's disease;
KW neurodegenerative disease.
KW
XX Homo sapiens.
XX
XX WO200068266-A1.
XX
XX 16-NOV-2000.
XX
XX 09-MAY-2000; 2000WO-US06707.
XX
XX 11-MAY-1999; 99US-0133423.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Becker GW, Hale JE, Heath WF, Johnstone EM, Little SP, Tu Y;
PI Yeh W, Yin T;
PI
XX WPI: 2001-016080/02.
XX
XX N-PSDB: AAC66921.
XX

PT New amyloid precursor protein proteases and nucleic acids useful for
PT identifying amyloid precursor protein protease inhibitors for treating
PT or preventing Alzheimer's disease and other neurodegenerative diseases
-
XX

Claim 1; Page 4-6; 82pp; English.

XX The present sequence is a human amyloid precursor protease protein.
XX Amyloid precursor protein builds up in the brain of individuals with
XX Alzheimer's disease, and the sequences of the invention can be used to
XX identify compounds which can be used to prevent and treat the disease. In
XX addition, they are suitable for use in the treatment of other
XX neurodegenerative diseases. Down's syndrome and hereditary cerebral
XX haemorrhage with amyloidosis of the Dutch-type (HCHWA-D).
XX

SQ Sequence 534 AA;

Query Match 15.2%; Score 239; DB 22; Length 534;

Best Local Similarity 27.5%; Pred. No. 6.3e-13;

Matches 71; Conservative 46; Mismatches 109; Indels 32; Gaps 9;

QY 20 IRMEPSPAMASLGQILFMSIISIIILAGATALLIGFGSGRHSITVTVASAGNIGEDG 79
Db 2 IIRGSPGPMG-----VHVGAAIGALWfcltgalevgvpedpvalvgtda 46
QY 80 ILSCYF--EPDIKLSDIYIQLKKEGVLGVHEFEKGEKDELSEQDEMFGRRTAVFADQYIV 137
Db 47 tlccsfspgfsfslaglnlwgldtkqlvhsfaegqd---qgsaayanrtalfpdliaq 102
QY 138 GNASRLKNNVQLTDAGTYKCYITTSKKGANLEKTKGA-FSMPEVNDYN-----ASSE 191
Db 103 gnasrlrlgrvrvadegsfctf-vslrldfgsaavslqvaaypskpsmtlepnkdlrpgdtv 161
QY 192 TLRCFAPRMFPQPTVYVMAQVDOGANFSEVSTSELSSENVTMKNVSVLVNVT-INNTY 250
Db 162 tlccssygygypaeavfw--qdgqgvyplcgnvts-qmanegldfvhslilrvlgangly 218
QY 251 SCMIENDIAKATGDIKVT 268
Db 219 sclvrnpvlgqdahesvt 236

RESULT 14

AAB87417

ID AAB87417 standard; Protein: 216 AA.

XX AAB87417;

Mon Jul 23 13:51:14 2001

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Page 13

job time: 119 sec

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